

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Lal, Preeti  
Bandman, Olga  
Hillman, Jennifer L.  
Shah, Purvi  
Corley, Neil C.
- (ii) TITLE OF THE INVENTION: NEW HUMAN REGULATORY PROTEINS
- (iii) NUMBER OF SEQUENCES: 74
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
  - (B) STREET: 3174 Porter Drive
  - (C) CITY: Palo Alto
  - (D) STATE: CA
  - (E) COUNTRY: USA
  - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: DOS
  - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/870,870
  - (B) FILING DATE: June 6, 1997
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Billings, Lucy J.
  - (B) REGISTRATION NUMBER: 36,749
  - (C) REFERENCE/DOCKET NUMBER: PF-0300 US
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 415-855-0555
  - (B) TELEFAX: 415-845-4166
  - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 260 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: None
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: U937NOT01

(B) CLONE: 187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Gln | Asn | Glu | Tyr | Ile | Glu | Leu | His | Arg | Lys | Arg | Tyr | Gly | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Leu | Asp | Tyr | His | Glu | Lys | Lys | Arg | Lys | Lys | Glu | Ser | Arg | Glu | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Asp | Arg | Ser | Lys | Lys | Ala | Lys | Lys | Met | Ile | Gly | Leu | Lys | Ala | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Tyr | His | Lys | Gln | Arg | His | Ala | Glu | Lys | Ile | Gln | Met | Lys | Lys | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Lys | Met | His | Glu | Lys | Arg | Asn | Thr | Lys | Gln | Lys | Asn | Asp | Glu | Lys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Thr | Pro | Gln | Gly | Ala | Val | Pro | Ala | Tyr | Leu | Leu | Asp | Arg | Glu | Gly | Gln |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Arg | Ala | Lys | Val | Leu | Ser | Asn | Met | Ile | Lys | Gln | Lys | Arg | Lys | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Ala | Gly | Lys | Trp | Glu | Val | Pro | Leu | Pro | Lys | Val | Arg | Ala | Gln | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Thr | Glu | Val | Leu | Lys | Val | Ile | Arg | Thr | Gly | Lys | Arg | Lys | Lys | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Ala | Trp | Lys | Arg | Met | Val | Thr | Lys | Val | Cys | Phe | Val | Gly | Asp | Gly | Phe |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Thr | Arg | Lys | Pro | Pro | Lys | Tyr | Glu | Arg | Phe | Ile | Arg | Pro | Met | Gly | Leu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Arg | Phe | Lys | Lys | Ala | His | Val | Thr | His | Pro | Glu | Leu | Lys | Ala | Thr | Phe |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Cys | Leu | Pro | Ile | Leu | Gly | Val | Lys | Lys | Asn | Pro | Ser | Ser | Pro | Leu | Tyr |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Thr | Thr | Leu | Gly | Val | Ile | Thr | Lys | Gly | Thr | Val | Ile | Glu | Val | Asn | Val |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ser | Glu | Leu | Gly | Leu | Val | Thr | Gln | Gly | Gly | Lys | Val | Ile | Trp | Gly | Lys |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Tyr | Ala | Gln | Val | Thr | Asn | Asn | Pro | Glu | Asn | Asp | Gly | Cys | Ile | Asn | Ala |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Val | Leu | Leu | Val |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 260 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: U937NOT01
- (B) CLONE: 2335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Lys | Asn | Thr | Val | Ser | Ser | Ala | Arg | Phe | Arg | Lys | Val | Asp | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Glu | Tyr | Asp | Glu | Asn | Lys | Phe | Val | Glu | Arg | Arg | Arg | Trp | Gly | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Ala | Arg | Ala | Arg | Ala | Pro | Ser | Glu | Gly | Glu | Val | Asp | Ser | Cys | Leu |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Arg | Gln | Gly | Asn | Met | Thr | Ala | Ala | Leu | Gln | Ala | Ala | Leu | Lys | Asn | Pro |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 50  |     | 55  |     | 60  |     |     |     |     |     |     |     |     |     |     |     |
| Pro | Ile | Asn | Thr | Lys | Ser | Gln | Ala | Val | Lys | Asp | Arg | Ala | Gly | Ser | Ile |
| 65  |     | 70  |     | 75  |     | 80  |     |     |     |     |     |     |     |     |     |
| Val | Leu | Lys | Val | Leu | Ile | Ser | Phe | Lys | Ala | Asn | Asp | Ile | Glu | Lys | Ala |
|     |     | 85  |     | 90  |     | 95  |     |     |     |     |     |     |     |     |     |
| Val | Gln | Ser | Leu | Asp | Lys | Asn | Gly | Val | Asp | Leu | Leu | Met | Lys | Tyr | Ile |
|     |     | 100 |     | 105 |     | 110 |     |     |     |     |     |     |     |     |     |
| Tyr | Lys | Gly | Phe | Glu | Ser | Pro | Ser | Asp | Asn | Ser | Ser | Ala | Met | Leu | Leu |
|     |     | 115 |     | 120 |     | 125 |     |     |     |     |     |     |     |     |     |
| Gln | Trp | His | Glu | Lys | Ala | Leu | Ala | Ala | Gly | Gly | Val | Gly | Ser | Ile | Val |
|     |     | 130 |     | 135 |     | 140 |     |     |     |     |     |     |     |     |     |
| Arg | Val | Leu | Thr | Ala | Arg | Lys | Thr | Val |     |     |     |     |     |     |     |
| 145 |     | 150 |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 185 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: None  
 (vii) IMMEDIATE SOURCE:  
 (A) LIBRARY: HUVENOB01  
 (B) CLONE: 36079

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | Ala | Asp | Thr | Leu | Leu | Ile | Val | Phe | Ile | Ser | Val | Cys | Thr | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Leu | Ala | Glu | Gly | Ile | Thr | Trp | Val | Leu | Val | Tyr | Arg | Thr | Asp | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Lys | Arg | Leu | Lys | Ala | Glu | Val | Glu | Lys | Gln | Ser | Lys | Lys | Leu | Glu |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Lys | Lys | Lys | Glu | Thr | Ile | Thr | Glu | Ser | Ala | Gly | Arg | Gln | Gln | Lys | Lys |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Ile | Glu | Arg | Gln | Glu | Lys | Leu | Lys | Asn | Asn | Arg | Asp | Leu |     |     |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |     |
| Ser | Met | Val | Arg | Met | Lys | Ser | Met | Phe | Ala | Ile | Gly | Phe | Cys | Phe | Thr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ala | Leu | Met | Gly | Met | Phe | Asn | Ser | Ile | Phe | Asp | Gly | Arg | Val | Val | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Leu | Pro | Phe | Thr | Pro | Leu | Ser | Tyr | Ile | Gln | Gly | Leu | Ser | His | Arg |
|     |     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Asn | Leu | Leu | Gly | Asp | Asp | Thr | Thr | Asp | Cys | Ser | Phe | Ile | Phe | Leu | Tyr |
|     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Ile | Leu | Cys | Thr | Met | Ser | Ile | Arg | Gln | Asn | Ile | Gln | Lys | Ile | Leu | Gly |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Leu | Ala | Pro | Ser | Arg | Ala | Ala | Thr | Lys | Gln | Ala | Gly | Gly | Phe | Leu | Gly |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Pro | Pro | Pro | Xaa | Ser | Gly | Lys | Phe | Ser |     |     |     |     |     |     |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 106 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None  
(vii) IMMEDIATE SOURCE:  
(A) LIBRARY: HUVESTB01  
(B) CLONE: 82709

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Thr | Asn | Asn | Met | Ser | Asp | Pro | Arg | Arg | Pro | Asn | Lys | Val | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Tyr | Lys | Pro | Pro | Pro | Ser | Glu | Cys | Asn | Pro | Ala | Leu | Asp | Asp | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Pro | Asp | Tyr | Met | Asn | Leu | Leu | Gly | Met | Ile | Phe | Ser | Met | Cys | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Met | Leu | Lys | Leu | Lys | Trp | Cys | Ala | Trp | Val | Ala | Val | Tyr | Cys | Ser |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Ile | Ser | Phe | Ala | Asn | Ser | Arg | Ser | Ser | Glu | Asp | Thr | Lys | Gln | Met |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Met | Ser | Ser | Phe | Met | Leu | Ser | Ile | Ser | Ala | Val | Val | Met | Ser | Tyr | Leu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gln | Asn | Pro | Gln | Pro | Met | Thr | Pro | Pro | Trp |     |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 166 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None  
(vii) IMMEDIATE SOURCE:  
(A) LIBRARY: LUNGNOT02  
(B) CLONE: 313727

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Ile | Pro | Pro | Asp | Ser | Trp | Gln | Pro | Pro | Asn | Val | Tyr | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Thr | Ser | Met | Gly | Ile | Ile | Val | Leu | Glu | Leu | Tyr | Trp | Lys | His | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Lys | Thr | Cys | Lys | Asn | Phe | Ala | Glu | Leu | Ala | Arg | Arg | Gly | Tyr | Tyr |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Asn | Gly | Thr | Lys | Phe | His | Arg | Ile | Ile | Lys | Asp | Phe | Met | Ile | Gln | Gly |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Asp | Pro | Thr | Gly | Thr | Gly | Arg | Gly | Gly | Ala | Ser | Ile | Tyr | Gly | Lys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Gln | Phe | Glu | Asp | Glu | Leu | His | Pro | Asp | Leu | Lys | Phe | Thr | Gly | Ala | Gly |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Ile | Leu | Ala | Met | Ala | Asn | Ala | Gly | Pro | Asp | Thr | Asn | Gly | Ser | Gln | Phe |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Val | Thr | Leu | Ala | Pro | Thr | Gln | Trp | Leu | Asp | Gly | Lys | His | Thr | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     |     |     |
| Phe | Gly | Arg | Val | Cys | Gln | Gly | Ile | Gly | Met | Val | Asn | Arg | Val | Gly | Met |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Glu | Thr | Asn | Ser | Gln | Asp | Arg | Pro | Val | Asp | Asp | Val | Lys | Ile | Ile |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Lys | Ala | Tyr | Pro | Ser | Gly |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     | 165 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTNOT05
- (B) CLONE: 965366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Lys | Gln | Gly | Gln | Met | Asp | Ala | Val | Arg | Ile | Met | Ala | Lys | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Val | Arg | Thr | Arg | Arg | Tyr | Val | Arg | Lys | Phe | Val | Leu | Met | Arg | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Ile | Gln | Ala | Val | Phe | Leu | Lys | Ile | Gln | Thr | Xaa | Lys | Phe | Asn | Xaa |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Xaa | Met | Ala | Gln | Ala | Met | Lys | Gly | Val | Asn | Lys | Ala | Met | Gly | Thr | Met |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn | Arg | Gln | Leu | Lys | Leu | Pro | Gln | Ile | Gln | Lys | Ile | Met | Met | Glu | Phe |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Glu | Arg | Gln | Ala | Glu | Ile | Met | Xaa | Met | Lys | Glu | Glu | Met | Met | Asn | Asp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Ile | Asp | Asp | Ala | Met | Gly | Asp | Glu | Glu | Asp | Glu | Glu | Glu | Ser | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Leu | Val | Phe | Gln | Gly | Leu | Asp | Glu | Leu | Gly | Leu | Ser | Leu | Thr | Asp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Leu | Ser | Asn | Leu | Pro | Ser | Thr | Gly | Gly | Ser | Leu | Ser | Val | Ala | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Gly | Lys | Lys | Ala | Glu | Ala | Ala | Ala | Ser | Ala | Leu | Ala | Asp | Ala | Asp |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ala | Asp | Leu | Glu | Glu | Arg | Leu | Lys | Asn | Leu | Arg | Arg | Asp |     |     |     |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNNOT16
- (B) CLONE: 1282071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Val | Arg | Ala | Ser | Phe | Glu | Asn | Asn | Cys | Glu | Ile | Gly | Cys | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Lys | Leu | Thr | Asn | Thr | Tyr | Cys | Leu | Val | Ala | Ile | Gly | Gly | Ser | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Phe | Tyr | Ser | Val | Phe | Glu | Gly | Glu | Leu | Ser | Asp | Thr | Ile | Pro | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | His | Ala | Ser | Ile | Ala | Gly | Cys | Arg | Ile | Ile | Gly | Arg | Met | Cys | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Asn | Arg | His | Gly | Leu | Leu | Val | Pro | Asn | Asn | Thr | Thr | Asp | Gln | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

PF-0300-3 CON

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Leu Gln His Ile Arg Asn Ser Leu Pro Asp Thr Val Gln Ile Arg Arg
      85          90          95
Val Glu Glu Arg Leu Ser Ala Leu Gly Asn Val Thr Thr Cys Asn Asp
      100        105        110
Tyr Val Ala Leu Val His Pro Asp Leu Asp Arg Glu Thr Glu Glu Ile
      115        120        125
Leu Ala Asp Val Leu Lys Val Glu Val Phe Arg Gln Thr Val Ala Asp
      130        135        140
Gln Val Leu Val Gly Ser Tyr Cys Val Phe Ser Asn Gln Gly Gly Leu
      145        150        155        160
Val His Pro Lys Thr Ser Ile Glu Asp Gln Asp Glu Leu Ser Ser Leu
      165        170        175
Leu Gln Val Pro Leu Val Ala Gly Thr Val Asn Arg Gly Ser Glu Val
      180        185        190
Ile Ala Ala Gly Met Val Val Asn Asp Trp Cys Ala Phe Cys Gly Leu
      195        200        205
Asp Xaa Thr Xaa Thr Glu Leu Ser Val Val Glu Ser Val Phe Lys Xaa
      210        215        220
Asn Glu Ala Gln Pro Xaa Thr Ile Ala Thr Ser Met Arg Asp Ser Leu
      225        230        235        240
Ile Asp Arg Leu Thr
      245

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(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LATRTUT02
- (B) CLONE: 1406755

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```

Met Lys Lys Val Arg Leu Lys Glu Leu Glu Ser Arg Leu Gln Gln Val
  1          5          10          15
Asp Gly Phe Glu Lys Pro Lys Leu Leu Leu Glu Gln Tyr Pro Thr Arg
      20        25        30
Pro His Ile Ala Ala Cys Met Leu Tyr Thr Ile His Asn Thr Tyr Asp
      35        40        45
Asp Ile Glu Asn Lys Val Val Ala Asp Leu Gly Cys Gly Cys Gly Val
      50        55        60
Leu Ser Ile Gly Thr Ala Met Leu Gly Ala Gly Leu Cys Val Gly Phe
      65        70        75        80
Asp Ile Asp Glu Asp Ala Leu Glu Ile Phe Asn Arg Asn Ala Glu Glu
      85        90        95
Phe Glu Leu Thr Asn Ile Asp Met Val Gln Cys Asp Val Cys Leu Leu
      100       105       110
Ser Asn Arg Met Ser Lys Ser Phe Asp Thr Val Ile Met Asn Pro Pro
      115       120       125
Phe Gly Thr Lys Asn Asn Lys Gly Thr Asp Met Ala Phe Leu Lys Thr
      130       135       140
Ala Leu Glu Met Ala Arg Thr Ala Val Tyr Ser Leu His Lys Ser Ser
      145       150       155       160

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Thr Arg Glu His Val Gln Lys Lys Ala Ala Glu Trp Lys Ile Lys Ile  
                    165                    170                    175  
Asp Ile Ile Ala Glu Leu Arg Tyr Asp Leu Pro Ala Ser Tyr Lys Phe  
                    180                    185                    190  
Leu Thr Lys Arg Asn Gln  
                    195

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 224 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: BLADTUT04

(B) CLONE: 1522948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ser Val Phe Gly Lys Leu Phe Gly Ala Gly Gly Gly Lys Ala Gly  
1                    5                    10                    15  
Lys Gly Gly Pro Thr Pro Gln Glu Ala Ile Gln Arg Leu Arg Asp Thr  
                    20                    25                    30  
Glu Glu Met Leu Ser Lys Lys Gln Glu Phe Leu Glu Lys Lys Ile Glu  
                    35                    40                    45  
Gln Glu Leu Thr Ala Ala Lys Lys His Gly Thr Lys Asn Lys Arg Ala  
50                    55                    60  
Ala Leu Gln Ala Leu Lys Arg Lys Lys Arg Tyr Glu Lys Gln Leu Ala  
65                    70                    75                    80  
Gln Ile Asp Gly Thr Leu Ser Thr Ile Glu Phe Gln Arg Glu Ala Leu  
                    85                    90                    95  
Glu Asn Ala Asn Thr Asn Thr Glu Val Leu Lys Asn Met Gly Tyr Ala  
                    100                    105                    110  
Ala Lys Ala Met Lys Ala Ala His Asp Asn Met Asp Ile Asp Lys Val  
                    115                    120                    125  
Asp Glu Leu Met Gln Asp Ile Ala Asp Gln Gln Glu Leu Ala Glu Glu  
130                    135                    140  
Ile Ser Thr Ala Ile Ser Lys Pro Val Gly Phe Gly Glu Glu Phe Asp  
145                    150                    155                    160  
Glu Asp Glu Leu Met Ala Glu Leu Glu Glu Leu Glu Gln Glu Xaa Leu  
                    165                    170                    175  
Asp Lys Asn Leu Leu Glu Ile Ser Gly Pro Glu Thr Val Pro Leu Pro  
                    180                    185                    190  
Asn Val Pro Ser Ile Ala Leu Pro Ser Lys Pro Ala Lys Lys Lys Glu  
                    195                    200                    205  
Glu Glu Asp Asp Asp Met Lys Glu Leu Glu Asn Trp Ala Gly Ser Met  
210                    215                    220

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

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(A) LIBRARY: BLADTUT04

(B) CLONE: 1554225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Arg | Gln | Ala | Asn | Arg | Gly | Thr | Glu | Ser | Lys | Lys | Met | Ser | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Leu | Phe | Thr | Leu | Thr | Tyr | Gly | Ala | Leu | Val | Thr | Gln | Leu | Cys | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Tyr | Glu | Asn | Asp | Glu | Asp | Val | Asn | Lys | Gln | Leu | Asp | Lys | Met | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Asn | Ile | Gly | Val | Arg | Leu | Ile | Glu | Asp | Phe | Leu | Ala | Arg | Ser | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Gly | Arg | Cys | His | Asp | Phe | Arg | Glu | Thr | Ala | Asp | Val | Ile | Ala | Lys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Val | Ala | Phe | Lys | Met | Tyr | Leu | Gly | Ile | Thr | Pro | Ser | Ile | Thr | Asn | Trp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Pro | Ala | Gly | Asp | Glu | Phe | Ser | Leu | Ile | Leu | Glu | Asn | Asn | Pro | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Asp | Phe | Val | Glu | Leu | Pro | Asp | Asn | His | Ser | Ser | Leu | Ile | Tyr | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Leu | Leu | Cys | Gly | Val | Leu | Arg | Gly | Ala | Leu | Glu | Met | Val | Gln | Met |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Ala | Val | Glu | Ala | Lys | Phe | Val | Gln | Asp | Thr | Leu | Lys | Gly | Asp | Gly | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Thr | Glu | Ile | Arg | Met | Arg | Phe | Ile | Arg | Arg | Ile | Glu | Asp | Asn | Leu | Pro |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ala | Gly | Glu | Glu |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 180 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 98 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: COLNTUT06

(B) CLONE: 1613785

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Lys | His | Ser | Cys | Arg | Lys | Val | Ala | Ser | Leu | Arg | Arg | Thr | Met |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Glu | Leu | Gly | Glu | Ala | Asp | Glu | Ala | Glu | Leu | Gln | Arg | Leu | Val | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Glu | Gln | Gln | Lys | Ala | Gln | Phe | Thr | Ala | Gln | Val | His | His | Phe | Met |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Leu | Cys | Trp | Asp | Lys | Cys | Val | Glu | Lys | Pro | Gly | Asn | Arg | Leu | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Arg | Thr | Glu | Asn | Cys | Leu | Ser | Ser | Cys | Val | Asp | Arg | Phe | Ile | Asp |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Thr | Thr | Leu | Ala | Ile | Thr | Ser | Arg | Phe | Ala | Gln | Ile | Val | Gln | Lys | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Gln |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:12:



(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 168 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None  
 (vii) IMMEDIATE SOURCE:  
 (A) LIBRARY: COLNNOT19  
 (B) CLONE: 1634175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Ala | Thr | Leu | Arg | Pro | Tyr | Leu | Ser | Ala | Val | Arg | Ala | Thr | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Gln | Ala | Ala | Leu | Cys | Leu | Glu | Asn | Phe | Ser | Ser | Gln | Val | Val | Glu | Arg |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| His | Asn | Lys | Pro | Glu | Val | Glu | Val | Arg | Ser | Ser | Lys | Glu | Leu | Leu | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Pro | Val | Thr | Ile | Ser | Arg | Asn | Glu | Lys | Glu | Lys | Val | Leu | Ile | Glu |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Ser | Ile | Asn | Ser | Val | Arg | Val | Ser | Ile | Ala | Val | Lys | Gln | Ala | Asp |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Glu | Ile | Glu | Lys | Xaa | Leu | Cys | His | Lys | Phe | Met | Arg | Phe | Met | Met | Met |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Ala | Glu | Asn | Phe | Phe | Ile | Leu | Arg | Lys | Pro | Val | Glu | Gly | Tyr |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Asp | Ile | Ser | Phe | Leu | Ile | Asn | Asn | Phe | His | Thr | Glu | Gln | Met | Tyr | Lys |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| His | Lys | Leu | Val | Asp | Phe | Val | Ile | His | Phe | Met | Glu | Glu | Ile | Asp | Lys |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | Ile | Ser | Glu | Met | Lys | Leu | Ser | Val | Asn | Ala | Arg | Ala | Arg | Ile | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ala | Glu | Glu | Phe | Leu | Lys | Asn | Phe |     |     |     |     |     |     |     |     |
|     |     |     |     | 165 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 247 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None  
 (vii) IMMEDIATE SOURCE:  
 (A) LIBRARY: BLADNOT05  
 (B) CLONE: 1675954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Cys | Asp | Gly | Gly | Thr | Ile | Pro | Lys | Arg | His | Glu | Leu | Val | Lys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Gly | Pro | Lys | Lys | Val | Glu | Lys | Val | Asp | Lys | Asp | Ala | Glu | Leu | Val | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Trp | Asn | Tyr | Cys | Thr | Leu | Ser | Gln | Glu | Ile | Leu | Arg | Arg | Pro | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Ala | Cys | Glu | Leu | Gly | Arg | Leu | Tyr | Asn | Lys | Asp | Ala | Val | Ile | Glu |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Leu | Leu | Asp | Lys | Ser | Ala | Glu | Lys | Ala | Leu | Gly | Lys | Ala | Ala | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

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```

His Ile Lys Ser Ile Lys Asn Val Thr Glu Leu Lys Leu Ser Asp Asn
      85                      90                      95
Pro Ala Trp Glu Gly Asp Lys Gly Asn Thr Lys Gly Asp Lys His Asp
      100                    105                    110
Asp Leu Gln Arg Ala Arg Phe Ile Cys Pro Val Val Gly Leu Glu Met
      115                    120                    125
Asn Gly Arg His Arg Phe Cys Phe Leu Arg Cys Cys Gly Cys Val Phe
      130                    135                    140
Ser Glu Arg Ala Leu Lys Glu Ile Lys Ala Glu Val Cys His Thr Cys
      145                    150                    155                    160
Gly Ala Ala Phe Gln Glu Asp Asp Val Ile Val Leu Asn Gly Thr Lys
      165                    170                    175
Glu Asp Val Asp Val Leu Lys Thr Arg Met Glu Glu Arg Arg Leu Arg
      180                    185                    190
Ala Xaa Trp Lys Arg Lys Gln Arg Asn Pro Arg Gln Gln Ser Leu Phe
      195                    200                    205
Gln Asn Gln Met Ser Val Lys Pro Gln Gly His Gln Lys Leu Arg Gln
      210                    215                    220
Gly Ser Leu Lys Lys Pro Ala Leu Ile Leu Glu Arg Arg Lys Pro Thr
      225                    230                    235                    240
Trp Leu Pro Lys Ala Gln Gln
      245

```

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: DUODNOT02
- (B) CLONE: 1707463

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```

Met Trp Arg Leu Leu Ala Arg Ala Ser Ala Pro Leu Leu Arg Val Pro
  1      5      10      15
Leu Ser Asp Ser Trp Ala Leu Leu Pro Ala Ser Ala Gly Val Lys Thr
      20      25      30
Leu Leu Pro Val Pro Ser Phe Glu Gly Glu Ser Leu Xaa Phe Ser Tyr
      35      40      45
Val Ser Ile Pro Glu Lys Pro Lys Leu Arg Phe Ile Glu Arg Ala Pro
      50      55      60
Leu Val Pro Lys Val Arg Arg Glu Pro Lys Asn Leu Ser Asp Ile Arg
      65      70      75      80
Gly Pro Phe Pro Leu Lys Leu Arg Ser Leu Gln Lys Ala Ile Phe Ala
      85      90      95
Ile Leu Ala Leu Gly Gly Gly Tyr Leu His Trp Gly His Phe Glu Met
      100      105      110
Met Arg Leu Thr Ile Asn Arg Ser Met Asp Pro Lys Asn Met Phe Ala
      115      120      125
Ile Trp Arg Val Pro Ala Pro Phe Lys Pro Ile Thr Arg Lys Ser Val
      130      135      140
Gly His Arg Met Gly Gly Lys Gly Ala Ile Asp His Tyr Val Thr
      145      150      155      160
Pro Val Lys Ala Gly Arg Leu Val Val Glu Met Gly Gly Arg Cys Glu
      165      170      175

```

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Phe Glu Glu Val Gln Gly Phe Leu Asp Gln Val Ala His Lys Leu Pro  
                  180                  185                  190  
Phe Ala Ala Lys Ala Val Ser Arg Gly Thr Leu Glu Lys Met Arg Lys  
                  195                  200                  205  
Asp Gln Glu Glu Arg Glu Arg Asn Asn Gln Asn Pro Trp Thr Phe Glu  
                  210                  215                  220  
Arg Ile Ala Thr Ala Asn Met Leu Gly Ile Arg Lys Val Leu Ser Pro  
225                  230                  235                  240  
Tyr Asp Leu Thr His Lys Gly Lys Tyr Trp Gly Lys Phe Tyr Met Pro  
                  245                  250                  255  
Lys Arg Val

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BLADNOT06
- (B) CLONE: 1720173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Ala Ala Ile Ala Ala Ser Glu Val Leu Val Asp Ser Ala Glu Glu  
1                  5                  10                  15  
Gly Ser Leu Ala Ala Ala Glu Leu Ala Ala Gln Lys Arg Glu Gln  
                  20                  25                  30  
Arg Leu Arg Lys Phe Arg Glu Leu His Leu Met Arg Asn Glu Ala Arg  
                  35                  40                  45  
Lys Leu Asn His Gln Glu Val Val Glu Glu Asp Lys Arg Leu Lys Leu  
50                  55                  60  
Pro Ala Asn Trp Glu Ala Lys Lys Ala Arg Leu Glu Trp Glu Leu Lys  
65                  70                  75                  80  
Glu Glu Glu Lys Lys Lys Glu Cys Ala Ala Arg Gly Glu Asp Tyr Glu  
                  85                  90                  95  
Lys Val Lys Leu Leu Glu Ile Ser Ala Glu Asp Ala Glu Arg Trp Glu  
                  100                  105                  110  
Arg Lys Lys Lys Arg Lys Asn Pro Asp Leu Gly Phe Ser Asp Tyr Ala  
115                  120                  125  
Ala Ala Gln Leu Arg Gln Tyr His Arg Leu Thr Lys Gln Ile Lys Pro  
130                  135                  140  
Asp Met Glu Thr Tyr Glu Arg Leu Arg Glu Lys His Gly Arg Arg Val  
145                  150                  155                  160  
Phe Pro Asn Ile Gln  
                  165

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: BRSTTUT08  
(B) CLONE: 1729330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Gly | Ser | Pro | Pro | Thr | Xaa | Pro | Ser | Pro | Ala | Ser | Asp | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Ser | Gly | Tyr | Val | Pro | Gly | Ser | Val | Ser | Ala | Ala | Phe | Val | Thr | Cys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Asn | Glu | Lys | Val | Ala | Lys | Glu | Ile | Ala | Arg | Ala | Val | Val | Glu | Lys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Leu | Ala | Ala | Cys | Val | Asn | Leu | Ile | Pro | Gln | Ile | Thr | Ser | Ile | Tyr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Trp | Lys | Gly | Lys | Ile | Glu | Glu | Asp | Ser | Glu | Val | Leu | Met | Met | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Thr | Gln | Ser | Ser | Trp | Ser | Gln | Leu |     |     |     |     |     |     |     |
|     |     |     |     | 85  |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: STOMTUT02  
(B) CLONE: 1746646

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Val | Phe | His | Asp | Glu | Val | Glu | Ile | Glu | Asp | Phe | Gln | Tyr | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Asp | Ser | Glu | Thr | Tyr | Phe | Tyr | Pro | Cys | Pro | Cys | Gly | Asp | Asn | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Ile | Thr | Lys | Glu | Asp | Leu | Glu | Asn | Gly | Glu | Asp | Val | Ala | Thr | Cys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Ser | Cys | Ser | Leu | Ile | Ile | Lys | Val | Ile | Tyr | Asp | Lys | Asp | Gln | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Cys | Gly | Glu | Thr | Val | Pro | Ala | Pro | Ser | Ala | Asn | Lys | Glu | Leu | Val |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Cys |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: LIVRTUT01  
(B) CLONE: 1753185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

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```

Met Leu Pro Ser Thr Ser Val Asn Ser Leu Val Gln Gly Asn Gly Val
 1          5          10          15
Leu Asn Ser Arg Asp Ala Ala Arg His Thr Ala Gly Ala Lys Arg Tyr
          20          25          30
Lys Tyr Leu Arg Arg Leu Phe Arg Phe Arg Gln Met Asp Phe Glu Phe
          35          40          45
Ala Ala Trp Gln Met Leu Tyr Leu Phe Thr Ser Pro Gln Arg Val Tyr
          50          55          60
Arg Asn Phe His Tyr Arg Lys Gln Thr Lys Asp Gln Trp Ala Arg Asp
65          70          75          80
Asp Pro Ala Phe Leu Val Leu Leu Ser Ile Trp Leu Cys Val Ser Thr
          85          90          95
Ile Gly Phe Gly Phe Val Leu Asp Met Gly Phe Phe Glu Thr Ile Lys
          100          105          110
Leu Leu Leu Trp Val Val Leu Ile Asp Cys Val Gly Val Gly Leu Leu
          115          120          125
Ile Ala Thr Leu Met Trp Phe Ile Ser Asn Lys Tyr Leu Val Lys Arg
130          135          140
Gln Ser Arg Asp Tyr Asp Val Glu Trp Gly Tyr Ala Phe Asp Val His
145          150          155          160
Leu Asn Ala Phe Tyr Pro Leu Leu Val Ile Leu His Phe Ile Gln Leu
          165          170          175
Phe Phe Ile Asn His Val Ile Leu Thr Asp Thr Phe Ile Gly Tyr Leu
          180          185          190
Val Gly Asn Thr Leu Trp Leu Val Ala Val Gly Tyr Tyr Ile Tyr Val
          195          200          205
Thr Phe Leu Gly Tyr Ser Ala Leu Pro Phe Leu Lys Asn Thr Val Ile
210          215          220
Leu Leu Tyr Pro Phe Ala Pro Leu Ile Leu Leu Tyr Gly Leu Ser Leu
225          230          235          240
Ala Leu Gly Trp Asn Phe Thr His Thr Leu Cys Ser Phe Tyr Lys Tyr
          245          250          255
Arg Val Lys

```

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNNOT08
- (B) CLONE: 1844162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

Met Ala Gly Ile Lys Ala Leu Ile Ser Leu Ser Phe Gly Gly Ala Ile
 1          5          10          15
Gly Leu Met Phe Leu Met Leu Gly Cys Ala Leu Pro Ile Tyr Asn Lys
          20          25          30
Tyr Trp Pro Leu Phe Val Leu Phe Tyr Ile Leu Ser Pro Ile Pro
          35          40          45
Tyr Cys Ile Ala Arg Arg Leu Val Asp Asp Thr Asp Ala Met Ser Asn
50          55          60
Ala Cys Lys Glu Leu Ala Ile Phe Leu Thr Thr Gly Ile Val Val Ser
65          70          75          80

```

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Ala Phe Gly Leu Pro Ile Val Phe Ala Arg Ala His Leu Ile Glu Trp  
85 90 95  
Gly Ala Cys Ala Leu Val Leu Thr Gly Asn Thr Val Ile Phe Ala Thr  
100 105 110  
Ile Leu Gly Phe Phe Leu Val Phe Gly Ser Asn Asp Asp Phe Ser Trp  
115 120 125  
Gln Gln Trp  
130

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNNOT08
- (B) CLONE: 1844338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Ala Asp Glu Ala Thr Arg Arg Val Val Ser Glu Ile Pro Val Leu  
1 5 10 15  
Lys Thr Asn Ala Gly Pro Arg Asp Arg Glu Leu Trp Val Gln Arg Leu  
20 25 30  
Lys Glu Glu Tyr Gln Ser Leu Ile Arg Tyr Val Glu Asn Asn Lys Asn  
35 40 45  
Ala Asp Asn Asp Trp Phe Arg Leu Glu Ser Asn Lys Glu Gly Thr Arg  
50 55 60  
Trp Phe Gly Lys Cys Trp Tyr Ile His Asp Leu Leu Lys Tyr Glu Phe  
65 70 75 80  
Asp Ile Glu Phe Asp Ile Pro Ile Thr Tyr Pro Thr Thr Ala Pro Glu  
85 90 95  
Ile Ala Val Pro Glu Leu Asp Gly Lys Thr Ala Lys Met Tyr Arg Gly  
100 105 110  
Gly Lys Ile Cys Leu Thr Asp His Phe Lys Pro Leu Trp Ala Arg Asn  
115 120 125  
Val Pro Lys Phe Gly Leu Ala His Leu Met Ala Leu Gly Leu Gly Pro  
130 135 140  
Trp Leu Ala Val Glu Ile Pro Asp Leu Ile Gln Lys Gly Val Ile Gln  
145 150 155 160  
His Lys Glu Lys Cys Asn Gln  
165

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGFET03
- (B) CLONE: 1853104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

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Met Ala Xaa Val Glu Glu Thr Leu Lys Arg Leu Gln Ser Gln Xaa Gly  
1 5 10 15  
Val Gln Gly Ile Ile Val Val Asn Thr Glu Gly Ile Pro Ile Lys Ser  
20 25 30  
Thr Met Asp Asn Pro Thr Thr Thr Gln Tyr Ala Ser Leu Met His Ser  
35 40 45  
Phe Ile Leu Lys Ala Arg Ser Thr Val Arg Asp Ile Asp Pro Gln Asn  
50 55 60  
Asp Leu Thr Phe Leu Arg Ile Arg Ser Lys Lys Asn Glu Ile Met Val  
65 70 75 80  
Ala Pro Asp Lys Asp Tyr Phe Leu Ile Val Ile Gln Asn Pro Thr Glu  
85 90 95

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSNOT18
- (B) CLONE: 1858616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Asn Tyr Met Pro Gly Thr Ala Ser Leu Ile Glu Asp Ile Asp Lys  
1 5 10 15  
Lys His Leu Val Leu Leu Arg Asp Gly Arg Thr Leu Ile Gly Phe Leu  
20 25 30  
Arg Ser Ile Asp Gln Phe Ala Asn Leu Val Leu His Gln Thr Val Glu  
35 40 45  
Arg Ile His Val Gly Lys Lys Tyr Gly Asp Ile Pro Arg Gly Ile Phe  
50 55 60  
Val Val Arg Gly Glu Asn Val Val Leu Leu Gly Glu Ile Asp Leu Glu  
65 70 75 80  
Lys Glu Ser Asp Thr Pro Leu Gln Gln Val Ser Ile Glu Glu Ile Leu  
85 90 95  
Glu Glu Gln Arg Val Glu Gln Gln Thr Lys Leu Glu Ala Glu Lys Leu  
100 105 110  
Lys Val Gln Ala Leu Lys Asp Arg Gly Leu Ser Ile Pro Arg Ala Asp  
115 120 125  
Thr Leu Asp Glu Tyr  
130

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: UCMCL5T01
- (B) CLONE: 1969807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

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```

Met Ala Ala Ser Ala Ala Arg Gly Ala Ala Ala Leu Arg Arg Ser Ile
 1          5          10          15
Asn Gln Pro Val Ala Phe Val Arg Arg Ile Pro Trp Thr Ala Ala Ser
          20          25          30
Ser Gln Leu Lys Glu His Phe Ala Gln Phe Gly His Val Arg Arg Cys
          35          40          45
Ile Leu Pro Phe Asp Lys Glu Thr Gly Phe His Arg Gly Leu Gly Trp
          50          55          60
Val Gln Phe Ser Ser Glu Glu Gly Leu Arg Asn Ala Leu Gln Gln Glu
          65          70          75          80
Asn His Ile Ile Asp Gly Val Lys Val Gln Val His Thr Arg Arg Pro
          85          90          95
Lys Leu Pro Gln Thr Ser Asp Asp Glu Lys Lys Asp Phe
          100          105

```

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: UCMCL5T01
- (B) CLONE: 1971003

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```

Met Ile Ser Leu Thr Asp Thr Gln Lys Ile Gly Met Gly Leu Thr Gly
 1          5          10          15
Phe Gly Val Phe Phe Leu Phe Phe Gly Met Ile Leu Phe Phe Asp Lys
          20          25          30
Ala Leu Leu Ala Ile Gly Asn Val Leu Phe Val Ala Gly Leu Ala Phe
          35          40          45
Val Ile Gly Leu Glu Arg Thr Phe Arg Phe Phe Phe Gln Lys His Lys
          50          55          60
Met Lys Ala Thr Gly Phe Phe Leu Gly Gly Val Phe Val Val Leu Ile
          65          70          75          80
Gly Trp Pro Leu Ile Gly Met Ile Phe Glu Ile Tyr Gly Phe Phe Leu
          85          90          95
Leu Phe Arg Gly Phe Phe Pro Val Val Gly Phe Ile Arg Arg Val
          100          105          110
Pro Val Leu Gly Ser Leu Leu Asn Leu Pro Gly Ile Arg Ser Phe Val
          115          120          125
Asp Lys Val Gly Glu Ser Asn Asn Met Val
          130          135

```

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: UCMCL5T01
- (B) CLONE: 1972328



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Gln | Gln | Gln | Gln | Gln | Leu | Arg | Asn | Leu | Arg | Asp | Phe | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Tyr | Asn | Arg | Met | Thr | Glu | Leu | Cys | Phe | Gln | Arg | Cys | Val | Pro | Ser |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | His | His | Arg | Ala | Leu | Asp | Ala | Glu | Glu | Glu | Ala | Cys | Leu | His | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Cys | Ala | Gly | Lys | Leu | Ile | His | Ser | Asn | His | Arg | Leu | Met | Ala | Ala | Tyr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | His | Leu | Met | Pro | Ala | Leu | Val | Gln | Arg | Arg | Ile | Ala | Asp | Tyr | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ala | Ala | Ser | Ala | Ala | Pro | Gly | Ile | Pro | Ala | Glu | Gln | Thr | Arg | Asp | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Ser | Gly | Ser |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 100 |

## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BEPINOT01
- (B) CLONE: 2057883

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Asn | Val | Ile | Asn | Thr | Val | Lys | Gly | Lys | Ala | Leu | Glu | Val | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Tyr | Leu | Thr | Pro | Val | Leu | Lys | Glu | Ser | Lys | Phe | Lys | Glu | Thr | Gly |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Ile | Thr | Pro | Glu | Glu | Phe | Val | Ala | Ala | Gly | Asp | His | Leu | Val | His |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| His | Cys | Pro | Thr | Trp | Gln | Trp | Ala | Thr | Gly | Glu | Glu | Leu | Lys | Val | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Tyr | Leu | Pro | Thr | Gly | Lys | Gln | Phe | Leu | Val | Thr | Lys | Asn | Val | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Cys | Tyr | Lys | Arg | Cys | Lys | Gln | Met | Glu | Tyr | Ser | Asp | Glu | Leu | Glu | Ala |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ile | Ile | Glu | Glu | Asp | Asp | Gly | Asp | Gly | Gly | Trp | Val | Asp | Thr | Tyr | His |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Thr | Gly | Ile | Thr | Gly | Ile | Thr | Glu | Ala | Val | Lys | Glu | Ile | Thr | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Glu | Asn | Lys | Asp | Asn | Ile | Arg | Leu | Gln | Asp | Cys | Ser | Ala | Leu | Cys | Glu |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Glu | Glu | Glu | Asp | Glu | Asp | Glu | Gly | Glu | Ala | Ala | Asp | Met | Glu | Glu | Tyr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Glu | Glu | Ser | Gly | Leu | Leu | Glu | Thr | Asp | Glu | Ala | Thr | Leu | Asp | Thr | Arg |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Lys | Ile | Val | Glu | Ala | Cys | Lys | Ala | Lys | Thr | Asp | Ala | Gly | Gly | Glu | Asp |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Ile | Leu | Gln | Thr | Arg | Thr | Tyr | Asp | Leu | Tyr | Ile | Thr | Tyr | Asp | Lys |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Tyr | Tyr | Gln | Thr | Pro | Arg | Leu | Trp | Leu | Phe | Gly | Tyr | Asp | Glu | Gln | Arg |
|     | 210 |     |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |

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Gln Pro Leu Thr Val Glu His Met Tyr Glu Asp Ile Ser Gln Asp His  
225 230 235 240  
Val Lys Lys Thr Val Thr Ile Glu Asn His Pro His Leu Pro Pro Pro  
245 250 255  
Pro Met Cys Ser Val His Pro Cys Arg His Ala Glu Val Met Lys Lys  
260 265 270  
Ile Ile Glu Thr Val Ala Glu Gly Gly Glu Leu Gly Val His Met  
275 280 285  
Tyr Leu Leu Ile Phe Leu Lys Phe Val Gln Ala Val Ile Pro Thr Ile  
290 295 300  
Glu Tyr Asp Tyr Thr Arg His Phe Thr Met  
305 310

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: ISLTNOT01
- (B) CLONE: 2075409

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Ser Arg Phe Leu Asn Val Leu Arg Ser Trp Leu Val Met Val Ser  
1 5 10 15  
Ile Ile Ala Met Gly Asn Thr Leu Gln Ser Phe Arg Asp His Thr Phe  
20 25 30  
Leu Tyr Glu Lys Leu Tyr Thr Gly Lys Pro Asn Leu Val Asn Gly Leu  
35 40 45  
Gln Ala Arg Thr Phe Gly Ile Trp Thr Leu Leu Ser Ser Val Ile Arg  
50 55 60  
Cys Leu Cys Ala Ile Asp Ile His Asn Lys Thr Leu Tyr His Ile Thr  
65 70 75 80  
Leu Trp Thr Phe Leu Leu Ala Leu Gly His Phe Leu Ser Glu Leu Phe  
85 90 95  
Val Tyr Gly Thr Ala Ala Pro Thr Ile Gly Val Leu Ala Pro Leu Met  
100 105 110  
Val Ala Ser Phe Ser Ile Leu Gly Met Leu Val Gly Leu Arg Tyr Leu  
115 120 125  
Glu Val Glu Pro Val Ser Arg Gln Lys Lys Arg Asn  
130 135 140

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRAITUT02
- (B) CLONE: 2095728

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Asp | Glu | Glu | Leu | Glu | Ala | Leu | Arg | Arg | Gln | Arg | Leu | Ala | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Gln | Ala | Lys | His | Gly | Asp | Pro | Gly | Asp | Ala | Ala | Gln | Gln | Glu | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | His | Arg | Glu | Ala | Glu | Met | Arg | Asn | Ser | Ile | Leu | Ala | Gln | Val | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Gln | Ser | Ala | Arg | Ala | Arg | Leu | Ser | Asn | Leu | Ala | Leu | Val | Lys | Pro |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Lys | Thr | Lys | Ala | Val | Glu | Asn | Tyr | Leu | Ile | Gln | Met | Ala | Arg | Tyr |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Gly | Gln | Leu | Ser | Glu | Lys | Val | Ser | Glu | Gln | Gly | Leu | Ile | Glu | Ile | Leu |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Lys | Lys | Val | Ser | Gln | Gln | Thr | Glu | Lys | Thr | Thr | Thr | Val | Lys | Phe | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Arg | Lys | Val | Met | Asp | Ser | Asp | Glu | Asp | Asp | Asp | Tyr |     |     |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRAITUT02
- (B) CLONE: 2100016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Tyr | Met | Leu | Pro | His | Leu | His | Asn | Gly | Trp | Gln | Val | Asp | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Ile | Leu | Ser | Glu | Glu | Asp | Arg | Val | Val | Val | Ile | Arg | Phe | Gly | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Trp | Asp | Pro | Thr | Cys | Met | Lys | Met | Asp | Glu | Val | Leu | Tyr | Ser | Ile |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Ala | Glu | Lys | Val | Lys | Asn | Phe | Ala | Val | Ile | Tyr | Leu | Val | Asp | Ile | Thr |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Val | Pro | Asp | Phe | Asn | Lys | Met | Tyr | Glu | Leu | Tyr | Asp | Pro | Cys | Thr |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Val | Met | Phe | Phe | Phe | Arg | Asn | Lys | His | Ile | Met | Ile | Asp | Leu | Gly | Thr |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Gly | Asn | Asn | Asn | Lys | Ile | Asn | Trp | Ala | Met | Glu | Asp | Lys | Gln | Glu | Met |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Asp | Ile | Ile | Glu | Thr | Val | Tyr | Arg | Gly | Ala | Arg | Lys | Gly | Arg | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Val | Val | Ser | Pro | Lys | Asp | Tyr | Ser | Thr | Lys | Tyr | Arg | Tyr |     |     |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

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(A) LIBRARY: KIDNNOT05

(B) CLONE: 2126751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Arg | Leu | Leu | Arg | Leu | Gly | Gly | Gly | Met | Pro | Gly | Leu | Gly | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Pro | Pro | Thr | Asp | Ala | Pro | Ala | Val | Asp | Thr | Ala | Glu | Gln | Val | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Ser | Ser | Leu | Ala | Leu | Leu | Lys | Met | Leu | Lys | His | Gly | Arg | Ala | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Pro | Met | Glu | Val | Met | Gly | Leu | Met | Leu | Gly | Glu | Phe | Val | Asp | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Thr | Val | Arg | Val | Ile | Asp | Val | Phe | Ala | Met | Pro | Gln | Ser | Gly | Thr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly | Val | Ser | Val | Glu | Ala | Val | Asp | Pro | Val | Phe | Gln | Ala | Lys | Met | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Met | Leu | Lys | Gln | Thr | Gly | Arg | Pro | Glu | Met | Val | Val | Gly | Trp | Tyr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| His | Ser | His | Pro | Gly | Phe | Gly | Cys | Trp | Leu | Ser | Gly | Val | Asp | Ile | Asn |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Gln | Gln | Ser | Phe | Glu | Ala | Leu | Ser | Glu | Arg | Ala | Val | Ala | Val | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Val | Asp | Pro | Ile | Gln | Ser | Val | Lys | Gly | Lys | Val | Val | Ile | Asp | Ala | Phe |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Arg | Leu | Ile | Asn | Ala | Asn | Met | Met | Val | Leu | Gly | His | Glu | Pro | Arg | Gln |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Thr | Thr | Ser | Asn | Leu | Gly | His | Leu | Asn | Lys | Pro | Ser | Ile | Gln | Ala | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | His | Gly | Leu | Asn | Arg | His | Tyr | Tyr | Ser | Ile | Thr | Ile | Asn | Tyr | Arg |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Lys | Asn | Glu | Leu | Glu | Gln | Lys | Met | Leu | Leu | Asn | Leu | His | Lys | Lys | Ser |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Trp | Met | Glu | Gly | Leu | Thr | Leu | Gln | Asp | Tyr | Ser | Glu | His | Cys | Lys | His |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Asn | Glu | Ser | Val | Val | Lys | Glu | Met | Leu | Glu | Leu | Ala | Lys | Asn | Tyr | Asn |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Lys | Ala | Val | Glu | Glu | Asp | Lys | Met | Thr | Pro | Glu | Gln | Leu | Ala | Ile |     |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Lys | Asn | Val | Gly | Lys | Gln | Asp | Pro | Lys | Arg | His | Leu | Glu | Glu | His | Val |
|     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |
| Asp | Val | Leu | Met | Thr | Ser | Asn | Ile | Val | Gln | Cys | Leu | Ala | Ala | Met | Leu |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Asp | Thr | Val | Val | Phe | Lys |     |     |     |     |     |     |     |     |     |     |
| 305 |     |     |     |     | 310 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: SININOT01

(B) CLONE: 2179882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

PF-0300-3 CON

```

Met Lys Ala Val Val Gln Arg Val Thr Arg Ala Ser Val Thr Val Gly
 1          5          10          15
Gly Glu Gln Ile Ser Ala Ile Gly Arg Gly Ile Cys Val Leu Leu Gly
          20          25          30
Ile Ser Leu Glu Asp Thr Gln Lys Glu Leu Glu His Met Val Arg Lys
          35          40          45
Ile Leu Asn Leu Arg Val Phe Glu Asp Glu Ser Gly Lys His Trp Ser
          50          55          60
Lys Ser Val Met Asp Lys Gln Tyr Glu Ile Leu Cys Val Ser Gln Phe
65          70          75          80
Thr Leu Gln Cys Val Leu Lys Gly Asn Lys Pro Asp Phe His Leu Ala
          85          90          95
Met Pro Thr Glu Gln Ala Glu Gly Phe Tyr Asn Ser Phe Leu Glu Gln
          100          105          110
Leu Arg Lys Thr Tyr Arg Pro Glu Leu Ile Lys Asp Gly Lys Phe Gly
          115          120          125
Ala Tyr Met Gln Val His Ile Gln Asn Asp Gly Pro Val Thr Ile Glu
130          135          140
Leu Glu Ser Pro Ala Pro Gly Thr Ala Thr Ser Asp Pro Lys Gln Leu
145          150          155          160
Ser Lys Leu Glu Lys Gln Gln Gln Arg Lys Glu Lys Thr Arg Ala Lys
          165          170          175
Gly Pro Ser Glu Ser Ser Lys Glu Arg Asn Thr Pro Arg Lys Glu Asp
          180          185          190
Arg Ser Ala Ser Ser Gly Ala Glu Gly Asp Val Ser Ser Glu Arg Glu
          195          200          205
Pro

```

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSNON01
- (B) CLONE: 2275119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```

Met Ala Lys His His Pro Asp Leu Ile Phe Cys Arg Lys Gln Ala Gly
 1          5          10          15
Val Ala Ile Gly Arg Leu Cys Glu Lys Cys Asp Gly Lys Cys Val Ile
          20          25          30
Cys Asp Ser Tyr Val Arg Pro Cys Thr Leu Val Arg Ile Cys Asp Glu
          35          40          45
Cys Asn Tyr Gly Ser Tyr Gln Gly Arg Cys Val Ile Cys Gly Gly Pro
          50          55          60
Gly Val Ser Asp Ala Tyr Tyr Cys Lys Glu Cys Thr Ile Gln Glu Lys
65          70          75          80
Asp Arg Asp Gly Cys Pro Lys Ile Val Asn Leu Gly Ser Ser Lys Thr
          85          90          95
Asp Leu Phe Tyr Glu Arg Lys Lys Tyr Gly Phe Lys Lys Arg
          100          105          110

```

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 264 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None  
 (vii) IMMEDIATE SOURCE:  
 (A) LIBRARY: PROSNON01  
 (B) CLONE: 2278093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Gly | Ser | Ser | Arg | Cys | Arg | Gly | Leu | Gln | Ile | Thr | Ala | Ser | Arg | 1   | 5   | 10  | 15  |
| Thr | Gly | Lys | Val | Tyr | Pro | Ala | Cys | His | Phe | Leu | Leu | Ala | Val | Ser | Ala | 20  | 25  | 30  |     |
| Gly | Ala | Arg | Gln | His | Val | Cys | Gly | Thr | Ala | Gln | Ser | Leu | Gly | Arg | Pro | 35  | 40  | 45  |     |
| Ala | Gly | Pro | Gly | Gly | Val | Thr | Gln | Phe | Gly | Asn | Lys | Tyr | Ile | Gln | Gln | 50  | 55  | 60  |     |
| Thr | Lys | Pro | Leu | Thr | Leu | Glu | Arg | Thr | Ile | Asn | Leu | Tyr | Pro | Leu | Thr | 65  | 70  | 75  | 80  |
| Asn | Tyr | Thr | Phe | Gly | Thr | Lys | Glu | Pro | Leu | Tyr | Glu | Lys | Asp | Ser | Ser | 85  | 90  | 95  |     |
| Val | Ala | Ala | Arg | Phe | Gln | Arg | Met | Arg | Glu | Glu | Phe | Asp | Lys | Ile | Gly | 100 | 105 | 110 |     |
| Met | Arg | Arg | Thr | Val | Glu | Gly | Val | Leu | Ile | Val | His | Glu | His | Arg | Leu | 115 | 120 | 125 |     |
| Pro | His | Val | Leu | Leu | Leu | Gln | Leu | Gly | Thr | Thr | Phe | Phe | Lys | Leu | Pro | 130 | 135 | 140 |     |
| Gly | Gly | Glu | Leu | Asn | Pro | Gly | Glu | Asp | Glu | Val | Glu | Gly | Leu | Lys | Arg | 145 | 150 | 155 | 160 |
| Leu | Met | Thr | Glu | Ile | Leu | Gly | Arg | Gln | Asp | Gly | Val | Leu | Gln | Asp | Trp | 165 | 170 | 175 |     |
| Val | Ile | Asp | Asp | Cys | Ile | Gly | Asn | Trp | Trp | Arg | Pro | Asn | Phe | Glu | Pro | 180 | 185 | 190 |     |
| Pro | Gln | Tyr | Pro | Tyr | Ile | Pro | Ala | His | Ile | Thr | Lys | Pro | Lys | Glu | His | 195 | 200 | 205 |     |
| Lys | Lys | Leu | Phe | Leu | Val | Gln | Leu | Gln | Glu | Lys | Ala | Leu | Phe | Ala | Val | 210 | 215 | 220 |     |
| Pro | Lys | Asn | Tyr | Lys | Leu | Val | Ala | Ala | Pro | Leu | Phe | Glu | Leu | Tyr | Asp | 225 | 230 | 235 | 240 |
| Asn | Ala | Pro | Gly | Tyr | Gly | Pro | Ile | Ile | Ser | Ser | Leu | Pro | Gln | Leu | Leu | 245 | 250 | 255 |     |
| Ser | Arg | Phe | Asn | Phe | Ile | Tyr | Asn |     |     |     |     |     |     |     |     | 260 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 153 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None  
 (vii) IMMEDIATE SOURCE:  
 (A) LIBRARY: TESTTUT02  
 (B) CLONE: 2345426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Gly | Ser | Arg | Leu | Glu | Thr | Val | Gly | Ser | Ile | Phe | Ser | Arg | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Asp | Leu | Val | Arg | Ala | Gly | Val | Leu | Lys | Glu | Lys | Pro | Leu | Trp | Phe |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Val | Tyr | Asp | Ala | Phe | Pro | Pro | Leu | Arg | Glu | Pro | Val | Phe | Gln | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Arg | Val | Arg | Tyr | Gly | Lys | Ala | Lys | Ala | Pro | Ile | Gln | Asp | Ile | Trp |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | His | Glu | Asp | Arg | Ile | Arg | Ala | Lys | Phe | Tyr | Ser | Val | Tyr | Gly | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Gly | Gln | Arg | Ala | Phe | Asp | Leu | Phe | Asn | Pro | Asn | Phe | Lys | Ser | Thr | Cys |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Gln | Arg | Phe | Val | Glu | Lys | Tyr | Thr | Glu | Leu | Gln | Lys | Leu | Gly | Glu | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Glu | Glu | Lys | Leu | Phe | Val | Glu | Thr | Gly | Lys | Ala | Leu | Leu | Gly | Arg |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Cys | His | Phe | Lys | Thr | Ser | Arg | Arg | Glu | Gly | Leu | Asn | Thr | Glu | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Thr | Phe | Pro | Gly | Asn | Pro | Asn | Thr |     |     |     |     |     |     |     |
| 145 |     |     |     |     | 150 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: ADRENOT07
- (B) CLONE: 2364523

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Arg | Gly | Val | Ile | Ala | Pro | Val | Gly | Glu | Ser | Leu | Arg | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Glu | Tyr | Leu | Gln | Pro | Ser | Ala | Lys | Arg | Pro | Asp | Ala | Asp | Val | Asp |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Gln | Arg | Leu | Val | Arg | Ser | Leu | Ile | Ala | Val | Gly | Leu | Gly | Val | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Leu | Ala | Phe | Ala | Gly | Arg | Tyr | Ala | Phe | Arg | Ile | Trp | Lys | Pro | Leu |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Gln | Val | Ile | Thr | Glu | Thr | Ala | Lys | Lys | Ile | Ser | Thr | Pro | Ser | Phe |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ser | Ser | Tyr | Tyr | Lys | Gly | Gly | Phe | Glu | Gln | Lys | Met | Ser | Arg | Arg | Glu |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ala | Gly | Leu | Ile | Leu | Gly | Val | Ser | Pro | Ser | Ala | Gly | Lys | Ala | Lys | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Thr | Ala | His | Arg | Arg | Val | Met | Ile | Leu | Asn | His | Pro | Asp | Lys | Gly |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Gly | Ser | Pro | Tyr | Val | Ala | Ala | Lys | Ile | Asn | Glu | Ala | Lys | Asp | Leu | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | Thr | Thr | Thr | Lys | His |     |     |     |     |     |     |     |     |     |     |
| 145 |     |     |     |     | 150 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 139 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None  
 (vii) IMMEDIATE SOURCE:  
 (A) LIBRARY: THP1NOT03  
 (B) CLONE: 2470912

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Ala | Val | Val | Phe | Val | Phe | Ser | Leu | Leu | Asp | Cys | Cys | Ala | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Phe | Leu | Ser | Val | Tyr | Phe | Ile | Ile | Thr | Leu | Ser | Asp | Leu | Glu | Cys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Tyr | Ile | Asn | Ala | Arg | Ser | Cys | Cys | Ser | Lys | Leu | Asn | Lys | Trp | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Pro | Glu | Leu | Ile | Gly | His | Thr | Ile | Val | Thr | Val | Leu | Leu | Leu | Met |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Leu | His | Trp | Phe | Ile | Phe | Leu | Leu | Asn | Leu | Pro | Val | Ala | Thr | Trp |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Asn | Ile | Tyr | Arg | Tyr | Ile | Met | Val | Pro | Ser | Gly | Asn | Met | Gly | Val | Phe |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Pro | Thr | Glu | Ile | His | Asn | Arg | Gly | Gln | Leu | Lys | Ser | His | Met | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Ala | Met | Ile | Lys | Leu | Gly | Phe | His | Leu | Leu | Cys | Phe | Phe | Met | Tyr |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Leu | Tyr | Ser | Met | Ile | Leu | Ala | Leu | Ile | Asn | Asp |     |     |     |     |     |
|     |     | 130 |     |     |     | 135 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 350 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None  
 (vii) IMMEDIATE SOURCE:  
 (A) LIBRARY: CONUTUT01  
 (B) CLONE: 2507014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Leu | Lys | Ala | Leu | Leu | Ser | Ser | Leu | Asn | Asp | Phe | Ala | Ser | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Phe | Ala | Glu | Ser | Trp | Asp | Asn | Val | Gly | Leu | Leu | Val | Glu | Pro | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Pro | His | Thr | Val | Asn | Thr | Leu | Phe | Leu | Thr | Asn | Asp | Leu | Thr | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Val | Met | Glu | Glu | Val | Leu | Gln | Lys | Lys | Ala | Asp | Leu | Ile | Leu | Ser |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | His | Pro | Pro | Ile | Phe | Arg | Pro | Met | Lys | Arg | Ile | Thr | Trp | Asn | Thr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Trp | Lys | Glu | Arg | Leu | Val | Ile | Arg | Ala | Leu | Glu | Asn | Arg | Val | Gly | Ile |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Tyr | Ser | Pro | His | Thr | Ala | Tyr | Asp | Ala | Ala | Pro | Gln | Gly | Val | Asn | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |



```

Trp Leu Ala Lys Gly Leu Gly Ala Cys Thr Ser Arg Pro Ile His Pro
      115                      120                      125
Ser Lys Ala Pro Asn Tyr Pro Thr Glu Gly Asn His Arg Val Glu Phe
      130                      135                      140
Asn Val Asn Tyr Thr Gln Asp Leu Asp Lys Val Met Ser Ala Val Lys
      145                      150                      155                      160
Gly Ile Asp Gly Val Ser Val Thr Ser Phe Ser Ala Arg Thr Gly Asn
      165                      170                      175
Glu Glu Gln Thr Arg Ile Asn Leu Asn Cys Thr Gln Lys Ala Leu Met
      180                      185                      190
Gln Val Val Asp Phe Leu Ser Arg Asn Lys Gln Leu Tyr Gln Lys Thr
      195                      200                      205
Glu Ile Leu Ser Leu Glu Lys Pro Leu Leu Leu His Thr Gly Met Gly
      210                      215                      220
Arg Leu Cys Thr Leu Asp Glu Ser Val Ser Leu Ala Thr Met Ile Asp
      225                      230                      235                      240
Arg Ile Lys Arg His Leu Lys Leu Ser His Ile Arg Leu Ala Leu Gly
      245                      250                      255
Val Gly Arg Thr Leu Glu Ser Gln Val Lys Val Val Ala Leu Cys Ala
      260                      265                      270
Gly Ser Gly Ser Ser Val Leu Gln Gly Val Glu Ala Asp Leu Tyr Leu
      275                      280                      285
Thr Gly Glu Met Ser His His Asp Thr Leu Asp Ala Ala Ser Gln Gly
      290                      295                      300
Ile Asn Val Ile Leu Cys Glu His Ser Asn Thr Glu Arg Gly Phe Leu
      305                      310                      315                      320
Ser Asp Leu Arg Asp Met Leu Asp Ser His Leu Glu Asn Lys Ile Asn
      325                      330                      335
Ile Ile Leu Ser Glu Thr Asp Arg Asp Pro Leu Gln Val Val
      340                      345                      350

```

## (2) INFORMATION FOR SEQ ID NO:38:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: U937NOT01
- (B) CLONE: 187

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```

GGAAAACAGA GGCTCGGAAC CGCTGCGTGG TTCTTGCTCT TCACTCGGCC GTTTTAAAGG      60
GTGACTCTTT CCTGTCCCGG CCTGCGTGGT GTGGGCTTGT GGGTCTTTGA GACCCGAAAA      120
TTGAGAGCGT TTTCGCACTC CAGCGGCTGC TCCTGGCGGC TCTGCGGCCG TCACCATGCC      180
ACAGAATGAA TATATTGAAT TACACCGTAA ACGCTATGGA TACCGTTTGG ATTACCATGA      240
GAAAAAGAGA AAGAAGGAAA GTCGAGAGGC TCATGACCGT TCAAAGAAGG CAAAGAAAAT      300
GATTGGTCTG AAGGCTAAGC TTTACCATAA ACAGCGTCAT GCTGAGAAAA TACAAATGAA      360
AAAGACTATC AAGATGCATG AAAAGAGAAA CACCAAACAA AAGAATGATG AAAAGACACC      420
ACAGGGAGCA GTACCTGCCT ATCTGCTGGA CAGAGAGGGA CAATCTCGAG CTAAAGTACT      480
TTCCAATATG ATTAAACAGA AAAGAAAAGA GAAGGCGGGA AAATGGGAAG TCCCTCTGCC      540
TAAAGTACGT GCCCAGGGAG AAACAGAAAGT ATTAAGAGTT ATTCGAACAG GAAAGAGAAA      600
GAAGAAGGCA TGGAAGAGAA TGGTACTAA AGTGTGCTTT GTTGGAGATG GCTTTACAAG      660
AAAACCACCT AAATATGAAA GATTCATCAG GCCAATGGGC TTGCGTTTCA AGAAAGCCCA      720
TGTAACACAT CCTGAACCTG AAGCCACCTT TTGCCCTACCA ATACTTGGTG TAAAGAAGAA      780
TCCCTCATCC CCACTGTATA CAACTTTGGG TGTTATTACC AAAGGTAAGT TCATTGAAGT      840
AAATGTGAGC GAATTGGGCC TTGTGACACA AGGAGGCAAA GTTATTTGGG GAAAATATGC      900
CCAGGTTACC AACAATCCTG AAAATGATGG ATGTATAAAT GCAGTCTTAC TGGTTTGACA      960

```

|             |            |            |            |            |            |      |
|-------------|------------|------------|------------|------------|------------|------|
| GCAATTTTCAT | ATATAATTAT | TGAGGACTAC | ACACCAATTG | AAGAACTGC  | CATTACTGTG | 1020 |
| ATGTTTCTGA  | ATACTACCAA | ACAGCCATAC | ATGTCTGCAA | TGAAGAGATT | TATTAAATTG | 1080 |
| TAAACATTAA  | AGTGGTCCAG | TTTTATAAAT | GGTNTTTATT | TTGAAATACG | CTTTGACCCC | 1140 |
| ATGTTCATAA  | AA         |            |            |            |            | 1152 |

## (2) INFORMATION FOR SEQ ID NO:39:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: U937NOT01
- (B) CLONE: 2335

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

|            |            |            |             |            |            |      |
|------------|------------|------------|-------------|------------|------------|------|
| AGGACGCCTC | AGAGCGGAAG | AGGGAAGTGA | ATCAGGCGCC  | GGGTAGTGGG | TTGCTGGGCT | 60   |
| GGGCTTGCTG | AGGTAGAGGC | AGCGCCAAGA | AGAGGCCTTT  | GCCGCTGGTC | GGGATTGGGA | 120  |
| TGTCGAAGAA | CACAGTGTCT | TCGGCCCGCT | TCCGGAAGGT  | GGACGTGGAT | GAATATGACG | 180  |
| AGAACAAGTT | CCTGGAACGA | AGAAGATGGG | GGCGACGGGC  | CAGGGCCCCG | GCCCCGAGCG | 240  |
| AGGGCGAGGT | GGACTCCTGC | CTGCGGCAAG | GAAACATGAC  | AGCTGCCCTA | CAGGCAGCTC | 300  |
| TGAAGAACCC | CCCTATCAAC | ACCAAGAGTC | AGGCAGTGAA  | GGACCGGGCA | GGCAGCATTG | 360  |
| TCTTGAAGGT | GCTCATCTCT | TTTAAAGCTA | ATGATATAGA  | AAAGGCAGTT | CAATCTCTGG | 420  |
| ACAAGAATGG | TGTGGATCTC | CTAATGAAGT | ATATTTATAA  | AGGATTTGAG | AGCCCGTCTG | 480  |
| ACAATAGCAG | TGCTATGTTA | CTGCAATGGC | ATGAAAAGGC  | ACTTGCTGCT | GGAGGAGTAG | 540  |
| GGTCCATTGT | TCGTGTCTTG | ACTGCAAGAA | AAACTGTGTA  | GTCTGGCAGG | AAGTGGATTA | 600  |
| TCTGCCTCGG | GAGTGGGAAT | TGCTGGTACA | AAGACCAAAA  | CAACCAAATG | CCACCGCTGC | 660  |
| CCTGTGGGTA | GCATCTGTTT | CTCTCAGCTT | TGCCTTCTTG  | CTTTTTCATA | TCTGTAAAGA | 720  |
| AAAAAATTAC | ATATCAGTTG | TCCTTTAATG | AAAATTGGGA  | TAATATAGAA | GAAATTGTGT | 780  |
| AAAATAGAAG | TGTTTCATCC | TTTCAAAACC | ATTTTCAGTGA | TGTTTATACC | AATCTGTATA | 840  |
| TAGTATAATT | TACATTCAAG | TTTAATTGTG | CAACTTTTAA  | CCCCTGTTGG | CTGGTTTTTT | 900  |
| GTTCTGTTTT | GTTTTGTATT | ATTTTTAACT | AATACTGAGA  | GATTTGGTCA | GAATTTGAGG | 960  |
| CCAGTTTCCT | AGCTCATTGC | TAGTCAGGAA | ATGATATTTA  | TAAAAAATAT | GAGAGACTGG | 1020 |
| CAGCTATTAA | CATTGCAAAA | CTGGACCATA | TTTCCCTTAT  | TTAATAAGCA | AAATATGTTT | 1080 |
| TTGGAATAAG | TGGTGGGTGA | ATACCACTGC | TAAGTTATAG  | CTTTGTTTTT | GCTTGCCTCC | 1140 |
| TGATTATCTG | TACTGTGGGT | TTAAGTATGC | TACTTTCTCT  | CAGCATCCAA | TAATCATGGC | 1200 |
| CCCTCAATTT | ATTTGTGGTC | ACCCAGGGTT | CAGAGCAAGA  | AGTCTTGCTT | TATACAAATG | 1260 |
| TATCCNTAAA | ATATCAGAGC | TTGTTGGGCA | TGAACATCAA  | ACTTTTGGTT | CCACTAATAT | 1320 |
| GGGCTCNGTT | TGGGAAAAAC | TGGC       |             |            |            | 1344 |

## (2) INFORMATION FOR SEQ ID NO:40:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1110 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: HUVENOB01
- (B) CLONE: 36079

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| CGATCTTCGG | GCTGTCAGAG | TTGGTCTGTT | ACTCGGTGGT | GGCGGAGTCT | ACGGAAGCCG | 60  |
| TTTTCGCTTC | ACTTTTCCTG | GCTGTAGAGC | GCTTTCCCCC | TGGCGGGTGA | GAGTGCAGAG | 120 |
| ACGAAGGTGC | GAGATGAGCA | CTATGTTTCG | GGACACTCTC | CTCATCGTTT | TTATCTCTGT | 180 |
| GTGCACGGCT | CTGCTCGCAG | AGGGCATAAC | CTGGGTCTCT | GTTTACAGGA | CAGACAAGTA | 240 |

|             |             |            |            |            |             |      |
|-------------|-------------|------------|------------|------------|-------------|------|
| CAAGAGACTG  | AAGGCAGAAG  | TGGAAAAACA | GAGTAAAAAA | TTGGAAAAGA | AGAAGGAAAC  | 300  |
| AATAACAGAG  | TCAGCTGGTC  | GACAACAGAA | AAAGAAAATA | GAGAGACAAG | AAGAGAAACT  | 360  |
| GAAGAATAAC  | AACAGAGATC  | TATCAATGGT | TCGAATGAAA | TCCATGTTTG | CTATTGGCTT  | 420  |
| TTGTTTACT   | GCCCTAATGG  | GAATGTTCAA | TTCCATATTT | GATGGTAGAG | TGGTGGCAAA  | 480  |
| GCTTCCTTTT  | ACCCCTCTTT  | CTTACATCCA | AGGACTGTCT | CATCGAAATC | TGCTGGGAGA  | 540  |
| TGACACCACA  | GACTGTTCCCT | TCATTTTCCT | GTATATTCTC | TGTACTATGT | CGATTTCGACA | 600  |
| GAACATTCAG  | AAGATTCTCG  | GCCTTGCCCC | TTCACGAGCC | GCCACCAAGC | AGGCAGGTGG  | 660  |
| ATTTCTTGGC  | CCACCACCTY  | CTTCTGGGAA | GTTCTCTTGA | ACTCAAGAAC | TCTTTATTTT  | 720  |
| CTATCATTTCT | TTCTAGACAC  | ACACACATCA | GACTGGCAAC | TGTTTTGTAG | CAAGAGCCAT  | 780  |
| AGGTAGCCTT  | ACTACTTGGG  | CCTCTTTCTA | GTTTTGAATT | ATTTCTAAGC | CTTTTGGGTA  | 840  |
| TGATTAGAGT  | GAAAATGGCA  | GCCAGCAAAC | TTGATAGTGC | TTTTGGTCCT | AGATGATTTT  | 900  |
| TATCAAATAA  | GTGGATTGAT  | TAGTTAAGTT | CAGGTAATGT | TTATGTAATG | AAAAACAAAT  | 960  |
| AGCATCCTTC  | TTGTTTCATT  | TACATAAGTA | TTTTCTGTGG | GACCGACTCT | CAAGGCACTG  | 1020 |
| TGTATGCCCT  | GCAAGTTGGC  | TGTCTATGAG | CATTTAGAGA | TTTAGAAGAA | AAATTTAGTT  | 1080 |
| TGTTTAACCC  | TTGTAAGTGT  | TTGTTTTGTT |            |            |             | 1110 |

## (2) INFORMATION FOR SEQ ID NO:41:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: HUVESTB01
- (B) CLONE: 82709

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| TGATCTGGCC | TTGCACTCGC | TATGTCCACT | AACAATATGT | CGGACCCACG | GAGGCCGAAT | 60  |
| AAAGTGCTGA | GGTACAAGCC | CCCGCCGAGC | GAATGTAACC | CGGCCTTGGA | CGACCCGACG | 120 |
| CCGGACTACA | TGAACCTGCT | GGGCATGATC | TTCAGCATGT | GCGGCCTCAT | GCTTAAGCTG | 180 |
| AAGTGGTGTG | CTTGGGTCGC | TGTCTACTGC | TCCTTCATCA | GCTTTGCCAA | CTCTCGGAGC | 240 |
| TCGGAGGACA | CGAAGCAAAT | GATGAGTAGC | TTCATGCTGT | CCATCTCTGC | CGTGGTGATG | 300 |
| TCCTATCTGC | AGAATCCTCA | GCCCATGACG | CCCCATGGT  | GATACCAGCC | TAGAAGGGTC | 360 |
| ACATTTTGGA | CCCTGTCTAT | CCACTAGGCC | TGGGCT     |            |            | 396 |

## (2) INFORMATION FOR SEQ ID NO:42:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1674 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGNOT02
- (B) CLONE: 313727

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| GCTTCTTCTC | GTCTCCCACC | CCAGCTTCCC | GGCATTGGAA | GAAGGGACCG | TCCTCTTCCT | 60  |
| TGTCTTGGCC | ACCCAAATCC | TGGTATCGAA | AGGGTTGAAC | GGACCGGAAG | TGTGCAGCAG | 120 |
| CGACGGGTCC | CCAGCTAATC | GACGCCGGAA | GTAGCAATTA | CTAGACAAGC | ATTCCGCCGC | 180 |
| CGGCTTCGCT | ATGGCGGCAA | TTCCCCAGA  | TTCTTGGCAG | CCACCCAACG | TTTACTTGGA | 240 |
| GACCAGCATG | GGAATCATTG | TGCTGGAGCT | GTAAGTGAAG | CATGCTCCAA | AGACCTGTAA | 300 |
| GAACCTTGCT | GAGTTGGCTC | GTCGAGGTTA | CTACAATGGC | ACAAAATTCC | ACAGAATTAT | 360 |
| CAAAGACTTC | ATGATCCAAG | GAGGTGACCC | AACAGGGACA | GGTCGAGGTG | GTGCATCTAT | 420 |
| CTATGGCAAA | CAGTTTGAAG | ATGAACCTCA | TCCAGACTTG | AAATTCACGG | GGGCTGGAAT | 480 |
| TCTCGCAATG | GCCAATGCGG | GGCCAGATAC | CAATGGCAGC | CAGTTCCTTG | TGACCCTCGC | 540 |

|            |            |            |             |            |            |      |
|------------|------------|------------|-------------|------------|------------|------|
| CCCCACCCAG | TGGCTTGACG | GCAAACACAC | CATTTTTTGGC | CGAGTGTGTC | AGGGCATAGG | 600  |
| AATGGTGAAT | CGCGTGGGAA | TGGTAGAAAC | AAACTCCCAG  | GACCGCCCTG | TGGACGACGT | 660  |
| GAAGATCATT | AAGGCATACC | CTTCTGGGTA | GACTTGCTAC  | CCTCTTGAGC | AGCTCTTCTG | 720  |
| AGATGGCCCC | AGTGAACCAG | CTTCTAGATG | ACATAGAATG  | ACATGTAATG | CTAAATTCAT | 780  |
| TTTGGGCTTT | GCAAGTCATG | AAGCTTAGGA | GGCCTGGCAT  | CTTGGGTGAG | TTAGAGATGG | 840  |
| AAGTACATTT | TAATAGGATG | CTTCTTTTCT | CTTCCCCCAG  | TGCCTAGGTT | GCCAGAGCAT | 900  |
| TTGCACAAAT | GCCCTGTGTT | ATCAATAGGT | GACTACTTAC  | TACACATGAA | CCATAATGCT | 960  |
| GCTTCTTGTC | CATGTCTGCT | CTGATATACG | TCGAACAATG  | TAGCAGCCAC | TGTCATTTCT | 1020 |
| CAGTGGTTTT | GCCTAACCAA | ACTTCTTCCT | AAGGAGATTT  | ATATTCTGGC | CTACACAGCA | 1080 |
| GTCTTGATG  | GCTGACAGCC | ACAGAATTCC | AAACCAAGTA  | GTGTCTGTCA | GCCCTCTTAA | 1140 |
| CTCTGTGCAC | GCCCTATTTT | AGTCTTTTAC | ATTTGTTCTT  | CTAGGGAATG | TATGCATCTC | 1200 |
| TATATATATT | TTCCCTCTCA | AAACCAGAAG | ATCAACAGTG  | CTGTTTCTGA | CACTTCAGAC | 1260 |
| ATCCCACGCA | AAGCCACATT | GAATTTTTCG | CAAATGAAAA  | ACACATCCAA | CAATCAAGTT | 1320 |
| TCTAAGAAGG | TGTCAAGTGG | GGAATAATAA | TAATGTATAA  | TAATCAAGAA | ATTAGTTTAT | 1380 |
| TAAAAGGAAG | CAGAAGCATT | GACCATTTTT | TCCAGAGAGAA | GAGGAGAAAT | CTGTAGTGAG | 1440 |
| CAAAGGACAG | ACCATGAATC | CTCCTTGAGA | AGTAGTACTC  | TCAGAAAGGA | GAAGCGCCAC | 1500 |
| TCAAGTTCTT | TTAACCCAAG | ACTTTAGAGA | AATTAGGTCC  | AAGATTTTTA | TATGTTCACT | 1560 |
| TGTTTATGTA | TAAAAATAAC | TTTCTGGATT | TTGTGGGGAG  | GAGCAGGAGA | GGAAGGAAGT | 1620 |
| TAATACCTAT | GTAATACATA | GAAACTTCCA | CAATAAAATG  | CCATTGATGG | TTGA       | 1674 |

## (2) INFORMATION FOR SEQ ID NO:43:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTNOT05
- (B) CLONE: 965366

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| GGGCGCCGGA  | AGACGCCAGA | GGAGCTACTG | CGGCAGAACC | AGAGGGCCCT | GAACCGTGCC | 60  |
| ATGCGGGAGC  | TGGACGCGCG | AGCGACAGAA | ACTAGAGACC | CAGGAGAAGA | AAATCATTCG | 120 |
| AGACATTAAG  | AAGATGGCCA | AGCAAGGCCA | GATGGATGCT | GTTCGCATCA | TGGCAAAAGA | 180 |
| CTTGGTGCGC  | ACCCGGCGCT | ATGTGCGCAA | GTTTGTATTG | ATGCGGGCCA | ACATCCAGGC | 240 |
| TGTGTTCCCTC | AAGATCCAGA | CANTNAAGTT | CAACAANTNG | ATGGCACAAG | CCATGAAGGG | 300 |
| TGTCAACAAG  | GCCATGGGCA | CCATGAACAG | ACAGCTGAAG | TTGCCCCAGA | TCCAGAAGAT | 360 |
| CATGATGGAG  | TTTGAGCGGC | AGGCAGAGAT | CATGGNTATG | AAGGAGGAGA | TGATGAATGA | 420 |
| TGCCATTGAT  | GATGCCATGG | GTGATGAGGA | AGATGAAGAG | GAGAGTGATG | CTTTGGTGTT | 480 |
| CCAGGGTCTT  | GATGAGCTGG | GACTTAGCCT | AACAGATGAG | CTGTCAAGCC | TCCCCTCAAC | 540 |
| TGGGGGCTCG  | CTTAGTGTGG | CTGCTGGTGG | GAAAAAAGCA | GAGGCCGCAG | CCTCAGCCCT | 600 |
| AGCTGATGCT  | GATGCAGACC | TGGAGGAACG | GCTTAAGAAC | CTGCGGAGGG | ACTGAGTGCC | 660 |
| CCTGCCACTC  | CGAGATAACC | AGTGGATGCC | CAGGATCTTT | TACCACAACC | CCTCTGTAAT | 720 |
| AAAAGAGANT  | A          |            |            |            |            | 731 |

## (2) INFORMATION FOR SEQ ID NO:44:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 916 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNNOT16
- (B) CLONE: 1282071

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| GGATGCGTGG | CGGGGAGCGC | CGGGCTCTCC  | CGGAAGTCTC | CCTGGACGGA | AGTGGAACG  | 60  |
| GAAACCTTTT | TAGGGAGTCC | AAGGTACAGT  | CGCCGCGTGC | GGACTTGTTA | CTGGTTACTT | 120 |
| GGCCTCATGG | CGGTCCGAGC | TTCGTTTCGAG | AACAACGTGT | AGATCGGCTG | CTTTGCCAAG | 180 |
| CTCACCAACA | CCTACTGTCT | GGTAGCGATC  | GGAGGCTCAG | AGAACTTCTA | CAGTGTGTTC | 240 |
| GAGGGCGAGC | TCTCCGATAC | CATCCCCGTG  | GTGCACGCGT | CTATCGCCGG | CTGCCGCATC | 300 |
| ATCGGGCGCA | TGTGTGTGGG | GAACAGGCAC  | GGTCTCCTGG | TACCCAACAA | TACCACCGAC | 360 |
| CAGGAGCTGC | AACACATTCG | CAACAGCCTC  | CCAGACACAG | TGCAGATTAG | GCGGGTGGAG | 420 |
| GAGCGGCTCT | CAGCCTTGGG | CAATGTCAAC  | ACCTGCAATG | ACTACGTGGC | CTTGGTCCAC | 480 |
| CCAGACTTGG | ACAGGGAGAC | AGAAGAAATT  | CTGGCAGATG | TGCTCAAGGT | GGAAGTCTTC | 540 |
| AGACAGACAG | TGGCCGACCA | GGTGCTAGTA  | GGAAGCTACT | GTGTCTTCAG | CAATCAGGGA | 600 |
| GGGCTGGTGC | ATCCCAAGAC | TTCAATTGAA  | GACCAGGATG | AGCTGTCCCT | TCTTCTTCAA | 660 |
| GTCCCCCTTG | TGGCGGGGAC | TGTGAACCGA  | GGCAGTGAGG | TGATTGCTGC | TGGGATGGTG | 720 |
| GTGAATGACT | GGTGTGCCCT | CTGTGGCCTG  | GACANAACCA | GNACAGAGCT | GTCAGTGGTG | 780 |
| GAGAGTGCTC | TCAAGNTGAA | TGAAGCCCAG  | CCTAGNACCA | TTGCCACCAG | CATGCGGGAT | 840 |
| TCCCTCATTG | ACAGGCTNAC | CTGAGTCAAC  | TTCCAAGTTG | TTCCATGGGC | TTCTGGNTCT | 900 |
| GGACTNTGNN | CAAACT     |             |            |            |            | 916 |

## (2) INFORMATION FOR SEQ ID NO:45:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LATRTUT02
- (B) CLONE: 1406755

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| GGCCTGGNGC | TTNCGGCACN | GGCCGAGGTG | CGGGTNGCCT | NCAGAGGTGC | GTGGTCGTGG | 60  |
| CGCGAGGGAT | CCTGAGGCTG | CTCCAGCAGT | GCGCNGANGC | NGTNTNCTGG | GGCGGGTTGG | 120 |
| GTTAGCCGGG | AGATCCTGTG | CCTTCAAACC | CTACGAGTCC | ATACTTTAAA | ACAAAATGAA | 180 |
| GAAAGTAAGG | CTTAAGGAAC | TAGAGAGTCG | CCTGCAACAA | GTGGATGGAT | TTGAAAAGCC | 240 |
| CAAGCTACTT | CTGGAACAGT | ATCCTACCAG | GCCGCACATT | GCAGCATGTA | TGCTCTATAC | 300 |
| AATCCATAAC | ACTTATGATG | ACATTGAAAA | TAAAGTCGTT | GCAGATCTAG | GATGTGGTTG | 360 |
| TGGAGTACTT | AGCATCGGAA | CTGCAATGTT | AGGAGCAGGG | TTGTGTGTTG | GATTTGACAT | 420 |
| AGATGAAGAC | GCATTGGAAA | TATTTAATAG | GAATGCAGAA | GAGTTTGAGT | TAACAAATAT | 480 |
| TGACATGGTT | CAATGTGATG | TGTGCTTATT | ATCTAACAGA | ATGTCCAAGT | CATTCGATAC | 540 |
| AGTAATTATG | AATCCTCCCT | TTGGGACCAA | AAATAATAAA | GGGACAGATA | TGGCTTTTCT | 600 |
| AAAGACTGCT | TTGGAAATGG | CAAGAACAGC | AGTATATTCC | TTACACAAAT | CCTCAACTAG | 660 |
| AGAACATGTT | CAAAAGAAAG | CTGCAGAATG | GAAAATCAAG | ATAGATATTA | TAGCAGAACT | 720 |
| TCGATATGAC | CTGCCAGCAT | CATACAAGTT | TCTGACAAAA | AGAAATCAGT | AAGTCTCTTG | 780 |
| ATTTTGGCTG | GTCTACATTC | GGTATTGAAA | AGCTTTCTTG |            |            | 820 |

## (2) INFORMATION FOR SEQ ID NO:46:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BLADTUT04
- (B) CLONE: 1522948

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

|            |            |            |            |            |            |    |
|------------|------------|------------|------------|------------|------------|----|
| GCGGGACTGG | GAGCGGNCGC | GGGNAGCCGA | CCCGAGCCGA | GCCGAGCCGA | GCCGAGCCGG | 60 |
|------------|------------|------------|------------|------------|------------|----|

|            |            |            |             |             |            |     |
|------------|------------|------------|-------------|-------------|------------|-----|
| AGCGGGCGGC | GAAGGCCGGC | GCGGCGAGCA | GCAACCATGT  | CGGTGTTTCGG | GAAGCTGTTC | 120 |
| GGGGCTGGAG | GGGGTAAGGC | CGGCAAGGGC | GGCCCGACCC  | CCCAGGAGGC  | CATCCAGCGG | 180 |
| CTGCGGGACA | CGGAAGAGAT | GTTAAGCAAG | AAACAGGAGT  | TCCTGGAGAA  | GAAAATCGAG | 240 |
| CAGGAGCTGA | CGGCCGCCAA | GAAGCACGGC | ACCAAAAACA  | AGCGCGCGGC  | CCTCCAGGCA | 300 |
| CTGAAGCGTA | AGAAGAGGTA | TGAGAAGCAG | CTGGCGCAGA  | TCGACGGCAC  | ATTATCAACC | 360 |
| ATCGAGTTCC | AGCGGGAGGC | CCTGGAGAAT | GCCAAACACCA | ACACCGAGGT  | GCTCAAGAAC | 420 |
| ATGGGCTATG | CCGCCAAGGC | CATGAAGGCG | GCCCATGACA  | ACATGGACAT  | CGATAAAGTT | 480 |
| GATGAGTTAA | TGCAGGACAT | TGCTGACCAG | CAAGAACTTG  | CAGAGGAGAT  | TTCAACAGCA | 540 |
| ATTTCGAAAC | CTGTAGGGTT | TGGAGAAGAG | TTTGACGAGG  | ATGAGCTCAT  | GGCGGAATTA | 600 |
| GAAGAACTAG | AACAGGAGGN | ACTAGACAAG | AATTTGCTGG  | AAATCAGTGG  | ACCCGAAACA | 660 |
| GTCCCTCTAC | CAAATGTTCC | CTCTATAGCC | CTACCATCAA  | AACCCGCCAA  | GAAGAAAGAA | 720 |
| GAGGAGGACG | ACGACATGAA | GGAATTGGAG | AAC'TGGGCTG | GATCCATGTA  | ATGGGGTCCA | 780 |
| GCGCTGGCTG | GGCCCAGACA | GACTGTGGTG | GCCTGCGCAN  | GAGCAGGCGT  | GTGCGTGTGT | 840 |
| GGGGCAGGCA | GGATGTGGTG | CAGGCAGGTT | CCATCGCTTT  | CGACTCTCAC  | TCCAAAGCAG | 900 |

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 848 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BLADTUT04
- (B) CLONE: 1554225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| GTCTTGTTGG | CTGAGGGGCA | GCGGCTTAGG | CTCCGGCGTC | TGCAGGGGTC | GCCGAGCTAA  | 60  |
| CCCGTGGCTA | GGCGAGTGGG | GCGGGGCGGC | CGGCACCATG | TCGAGGCAGG | CGAACCGTGG  | 120 |
| CACCGAGAGC | AAGAAAATGA | GCTCTGAGCT | CTTCACCCTG | ACCTATGGTG | CCCTGGTCAC  | 180 |
| CCAGCTATGT | AAGGACTATG | AAAATGATGA | AGATGTGAAT | AAACAGCTGG | ACAAAATGGG  | 240 |
| CTTTAACATT | GGAGTCCGGC | TGATTGAAGA | TTTCTTGGCT | CGGTCAAATG | TTGGGAGGTG  | 300 |
| CCATGACTTT | CGGGAAACTG | CGGATGTCAT | TGCCAAGGTG | GCGTTCAAGA | TGTACTTGGG  | 360 |
| CATCACTCCA | AGCATTACTA | ATTGGAGCCC | AGCTGGTGAT | GAATTCCTCC | TCATTTTGGG  | 420 |
| AAATAACCCC | TTGGTGGACT | TTGTGGAAT  | TCCTGATAAC | CACTCATCCC | TTATTTATTC  | 480 |
| CAATCTCTTG | TGTGGGGTGT | TGCGGGGAGC | TTTGGAGATG | GTCCAGATGG | CTGTGGAGGC  | 540 |
| CAAGTTTGTC | CAGGACACCC | TGAAAGGAGA | CGGTGTGACA | GAAATCCGGA | TGAGATTTCAT | 600 |
| CAGGCGGATT | GAGGACAATC | TTCCAGCTGG | AGAGGAATAA | CCATCCCTAC | AACTCGAGGA  | 660 |
| TAGCCATCAG | GAGCACTGTT | GGAATCAGCA | GGCCTCTGTG | CTCCCTCTGC | CCTCCAGAAC  | 720 |
| TCAGTGACTC | TTGAACATGG | ATGTTATATA | TTCTTATAAC | CTGTTTCCAT | TCTCCATTCA  | 780 |
| AATAAAGAGC | AGACTGCGAT | ATAGTCCATT | TAACCCATGT | GTGCACATGT | GGGGGCGANN  | 840 |
| NTTTGTTT   |            |            |            |            |             | 848 |

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNTUT06
- (B) CLONE: 1613785

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

|            |            |            |            |            |            |    |
|------------|------------|------------|------------|------------|------------|----|
| CCGTCGCGCA | TGCGCAAACA | CAGCTGTCCG | AAGGTGGCGA | GCCTGAGGCG | AACAATGGCG | 60 |
|------------|------------|------------|------------|------------|------------|----|

|             |            |            |             |             |            |     |
|-------------|------------|------------|-------------|-------------|------------|-----|
| GAGCTGGGCG  | AAGCCGATGA | AGCGGAGTTG | CAGCGCCTGG  | TGGCCGCCGA  | GCAGCAGAAG | 120 |
| GCGCAGTTTA  | CTGCACAGGT | GCATCACTTC | ATGGAGTTAT  | GT'TGGGATAA | ATGTGTGGAG | 180 |
| AAGCCAGGGA  | ATCGCCTAGA | CTCTCGCACT | GAAAAATTGTC | TCTCCAGCTG  | TGTAGACCGC | 240 |
| TTCATTGACA  | CCACTCTTGC | CATCACCAGT | CGGTTTGCCC  | AGATTGTACA  | GAAAGGAGGG | 300 |
| CAGTAGGCCA  | TCCCCCAGGA | GAATGACAGA | AGCAAAGGAC  | TTGTTACTAA  | GCAGATTTAA | 360 |
| GGGTCAGTGG  | GGGAAGGCTA | TCAACCCATT | GTCAGATCAG  | CATCAGGCTG  | TTATCAAGTC | 420 |
| TGTTGGTGTCT | AAAAAGTAAA | AGATGAAATG | TTCAA       |             |            | 455 |

## (2) INFORMATION FOR SEQ ID NO:49:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNNOT19
- (B) CLONE: 1634175

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| CTGCGCTTCT | CGCGAAANGG | CAGGCATCGC | GGGGCTGGCC | ACTTCCGTAC | TTCCGCTTTC | 60  |
| CGGCCAGCC  | AGCGCCCGCG | ATGACTGCCA | CTCTCCGCCC | CTACCTGAGT | GCCGTGCGGG | 120 |
| CCACATTGCA | GGCTGCCCTC | TGCCTGGAGA | ACTTCTCCTC | CCAGGTGTGT | GAACGACACA | 180 |
| ACAAGCCGGA | AGTGGAAAGT | AGGAGTAGCA | AAGAGCTCCT | GTTACAACCT | GTGACCATCA | 240 |
| GCAGGAATGA | GAAGGAAAAG | GTTCTGATTG | AGGGCTCCAT | CAACTCTGTC | CGGGTCAGCA | 300 |
| TTGCTGTGAA | ACAGGCTGAT | GAGATCGAGA | AGNTTTTGTG | CCACAAGTTC | ATGCGCTTCA | 360 |
| TGATGATGCG | AGCAGAGAAC | TTCTTTATCC | TTCGAAGGAA | GCCTGTGGAG | GGGTATGATA | 420 |
| TCAGCTTTCT | GATCAACAAC | TTTCACACAG | AGCAGATGTA | CAAACACAAG | TTGGTGGACT | 480 |
| TTGTGATCCA | CTTCATGGAG | GAGATTGACA | AGGAGATCAG | TGAGATGAAG | CTGTCAGTCA | 540 |
| ATGCCCGTGC | CCGCATTGTG | GCTGAAGAGT | TCCTTAAGAA | TTTTTAAACC | ATCTGGCTGG | 600 |
| ATCTCGTGGC | CTTCCCCCTG | AGACTACCCA | TGTCTTCAAG | GAGGCGTCCT | GGNGTCACTT | 660 |
| CCCGAGCAGC | GCGGCGGCGG | CAGGAAGTTG | GGTTGGGGTG | GGCATTGTAT | GCGGGAGGTG | 720 |
| GGTGGTGTGC | TTGCTAGCTG | GGCAAGAAAG | C          |            |            | 751 |

## (2) INFORMATION FOR SEQ ID NO:50:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 856 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BLADNOT05
- (B) CLONE: 1675954

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| TGCTGGCTCT | GACTCCCGTC | CTGCGATGGG | TTGCGACGGG | GGAACAATCC | CCAAGAGGCA | 60  |
| TGAACTGGTG | AAGGGGCCGA | AGAAGGTTGA | GAAGGTCGAC | AAAGATGCTG | AATTAGTGGC | 120 |
| CCAATGGAAC | TATTGTACTC | TAAGTCAGGA | AATATTAAGA | CGACCAATAG | TTGCCTGTGA | 180 |
| ACTTGGCAGA | CTTTATAACA | AAGATGCCGT | CATTGAATTT | CTCTTGAGCA | AATCTGCAGA | 240 |
| AAAGGCTCTT | GGGAAGGCAG | CATCTCACAT | TAAAAGCATT | AAGAATGTGA | CAGAGCTGAA | 300 |
| GCTTCTGTAT | AATCCTGCCT | GGGAAGGGGA | TAAAGGAAAC | ACTAAAGGTG | ACAAGCACGA | 360 |
| TGACCTCCAG | CGGGCGCGTT | TCATCTGCCC | CGTTGTGGGC | CTGGAGATGA | ACGCCGACA  | 420 |
| CAGGTTCTGC | TTCTTTCGGT | GCTGCGGCTG | TGTGTTTTCT | GAGCGAGCCT | TGAAAGAGAT | 480 |
| AAAAGCGGAA | GTTTGCCACA | CGTGTGGGGC | TGCCTTCCAG | GAGGATGATG | TCATCGTGCT | 540 |
| CAATGGCACC | AAGGAGGATG | TGGACGTGCT | GAAGACAAGG | ATGGAGGAGA | GAAGGCTGAG | 600 |
| AGCGAANTGG | AAAAGAAAAC | AAAGAAAACC | AAGGCAGCAG | AGTCTGTTTC | AAAACCAGAT | 660 |

|            |            |             |             |            |            |     |
|------------|------------|-------------|-------------|------------|------------|-----|
| GTCAGTGAAG | CCCCAGGGCC | ATCAAAAAGTT | AAGACAGGGA  | AGCCTGAAGA | AGCCAGCCTT | 720 |
| GATTCTAGAG | AGAAGAAAAC | CAACTTGGCT  | CCCCAAAAGCA | CAGCAATGAA | TGAGAGCTCT | 780 |
| TCTGGAAAAG | CTGGGAAGCC | TCCGTGTGGA  | GCCACAAAGA  | GGTCCATCGC | TGACAGTGAA | 840 |
| GAATCGGAGG | CCTACA     |             |             |            |            | 856 |

## (2) INFORMATION FOR SEQ ID NO:51:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: DUODNOT02
- (B) CLONE: 1707463

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

|            |             |            |             |            |            |      |
|------------|-------------|------------|-------------|------------|------------|------|
| GGGTGAACAC | AACTTCCGGC  | CCCACTGAGC | GGTGTCCCTGA | GCCGATTACA | GCTAGGTAGT | 60   |
| GGAGCGCCGC | TGCTTACCTG  | GGTGCAGGAG | ACAGCCGGAG  | TCGCTGGGGG | AGCTCCGCGC | 120  |
| CGCCGGACGC | CCGTGACCAT  | GTGGAGGCTG | CTGGCTCGCG  | CTAGTGCGCC | GCTCCTGCGG | 180  |
| GTGCCCTTGT | CAGATTCCCTG | GGCACTCCTC | CCC GCCAGTG | CTGGCGTAAA | GACACTGCTC | 240  |
| CCAGTACCAA | GTTTTGAAGG  | TGAGAGCTTG | TNTTTTCTCCT | ATGTTTCCAT | TCCTGAAAAA | 300  |
| CCCAAGCTTA | GATTTATTGA  | AAGGGCACCA | CTTGTGCCAA  | AAGTAAGAAG | AGAACCTAAA | 360  |
| AATTTAAGTG | ACATACGGGG  | ACCGTTCCCA | CTGAAGCTAC  | GGAGTTTACA | GAAGGCAATT | 420  |
| TTTGCAATCT | TGGCATTGGG  | TGGTGGCTAC | CTGCATTGGG  | GCCACTTTGA | AATGATGCGC | 480  |
| CTGACAATCA | ACCGCTCTAT  | GGACCCCAAG | AACATGTTTG  | CCATATGGCG | AGTACCAGCC | 540  |
| CCTTTCAAGC | CCATCACTCG  | CAAAAGTGTT | GGGCATCGCA  | TGGGGGGAGG | CAAAGGTGCT | 600  |
| ATTGACCACT | ACGTGACACC  | TGTGAAGGCT | GGCCGCCCTTG | TTGTAGAGAT | GGGTGGGCGT | 660  |
| TGTGAATTTG | AAGAAGTGCA  | AGGTTTCCTT | GACCAGGTTG  | CCCACAAGTT | GCCCTTCGCA | 720  |
| GCAAAGGCTG | TGAGCCGCGG  | GACTCTAGAG | AAGATGCGAA  | AAGATCAAGA | GGAAAGAGAA | 780  |
| CGTAACAACC | AGAACCCCTG  | GACATTTGAG | CGAATAGCCA  | CTGCCAACAT | GCTGGGCATA | 840  |
| CGGAAAGTAC | TGAGCCCAT   | TGACTTGACC | CACAAGGGGA  | AATACTGGGG | CAAGTTCTAC | 900  |
| ATGCCCAAAC | GTGTGTAGTG  | AGTGTAGGAG | ATAACTGTAT  | ATAGGCTACT | GAAAGAAGGA | 960  |
| TTCTGCATTT | CTATTCCTCT  | CAGCCTACCC | ACTGAAAGTCT | TTGGGTAGCT | CTTAAGCCAT | 1020 |
| AACTAAGGAG | CAGCATTTGA  | GTAGATTTCT | GAAAAACAAT  | GTTATTTGTT | GATTTAAAAA | 1080 |
| GAAACTGTA  | TTTTTATTAA  | ATAAAATTTA | AACATCACTT  | CAGGG      |            | 1125 |

## (2) INFORMATION FOR SEQ ID NO:52:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 595 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BLADNOT06
- (B) CLONE: 1720173

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| CCGGAAGTGG | GAAGAGAGAA | AGGTTGTGAT | GGCGGCTATA | GCTGCATCCG | AGGTGCTGGT | 60  |
| GGACAGCGCG | GAGGAGGGGT | CCCTCGCTGC | GGCGGCGGAG | CTGGCCGCTC | AGAAGCGCGA | 120 |
| ACAGAGACTG | CGCAAATTCC | GGGAGCTGCA | CCTGATGCGG | AATGAAGCTC | GTAAATTAAA | 180 |
| TCACCAGGAA | GTTGTGGAAG | AAGATAAAAG | ACTAAAATTA | CCTGCAAATT | GGGAAGCCAA | 240 |
| AAAAGCTCGT | TTGGAGTGGG | AACTAAAGGA | AGAGGAAAAG | AAAAAGGAAT | GTGCGGCAAG | 300 |
| AGGAGAAGAC | TATGAGAAAG | TGAAGTTGCT | GGAGATCAGT | GCAGAAGATG | CAGAAAGATG | 360 |
| GGAGAGGAAA | AAGAAGAGGA | AAAACCTCTG | TCTGGGATTT | TCAGATTATG | CTGCTGCCCA | 420 |
| GTTACGCCAG | TATCATCGGT | TGACCAAGCA | GATCAAACCT | GACATGGAAA | CATATGAGAG | 480 |



|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ACTGAGAGAA | AAACATGGGA | GAAGAGTTTT | TCCCAACATC | CAATAGTCTT | CTTCATGGAA | 540 |
| CACATGTGCC | TTCCACAGAG | GAAATTGACA | GGATGGTCAT | GGNTCTGGAA | AAACA      | 595 |

## (2) INFORMATION FOR SEQ ID NO:53:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTTUT08
- (B) CLONE: 1729330

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| CTTGCTGACC | ATGGCCTCTG | GAAGCCCTCC | GACCCANCCC | TCGCCGGCCT | CGGATTCCGG | 60  |
| CTCTGGCTAC | GTTCGGGGCT | CGGTCTCTGC | AGCCTTTGTT | ACTTGCCCCA | ACGAGAAGGT | 120 |
| CGCCAAGGAG | ATCGCCAGGG | CCGTGGTGGA | GAAGCGCCTA | GCAGCCTGCG | TCAACCTCAT | 180 |
| CCCTCAGATT | ACATCCATCT | ATGAGTGGA  | AGGGAAGATC | GAGGAAGACA | GTGAGGTGCT | 240 |
| GATGATGATT | AAAACCCAAA | GTTCTTGGTC | CCAGCTTTGA | CAGATTTTGT | TCGTTCTGTG | 300 |
| CACCCTTACG | AAGTGGCCGA | GGTAATTGCA | TTGCCTGTGG | AACAGGGGAA | CTTTCCGTAC | 360 |
| CTGCAGTGGG | TGCGCCAGGT | CACAGAGTCA | GTTTCTGACT | CTATCACAGT | CCTGCCATGA | 420 |
| TGAGCCCC   |            |            |            |            |            | 428 |

## (2) INFORMATION FOR SEQ ID NO:54:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: STOMTUT02
- (B) CLONE: 1746646

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

|            |            |            |             |             |            |     |
|------------|------------|------------|-------------|-------------|------------|-----|
| CGGCGAAGTT | AAACCCTCGG | AGCTGGCCTC | GGA CTGCTGG | GGCGTTACCC  | CTTCGGCCAC | 60  |
| CCCCGCTGAC | CATGGCAGTG | TTTCATGACG | AGGTGGAAAT  | CGAGGACTTC  | CAATATGACG | 120 |
| AGGACTCGGA | GACGTATTTC | TATCCCTGCC | CATGTGGAGA  | TAAC TTCTCC | ATCACCAAGG | 180 |
| AAGATTTGGA | GAATGGGGAA | GACGTGGCAA | CGTGTCTAG   | CTGCTCTCTC  | ATTATAAAG  | 240 |
| TGATTTATGA | CAAAGATCAG | TTTGTGTGTG | GAGAAACAGT  | CCCAGCCCCCT | TCAGCCAACA | 300 |
| AAGAATTAGT | TAAATGCTGA | AGAAGCCTTC | AGGAATCCAA  | ATCCTGAACA  | TTTGGAATGA | 360 |
| GCCCAGATAG | AAATATCGAA | TGCAAAGCTA | CTGGCTTCAC  | AGAGACAACC  | ATTTATGATT | 420 |
| TGCTGTTCTG | TAAGAGTGTG | GATTCTTTCT | ATCAACTGCT  | GATATCATCT  | TCAGGAAGCA | 480 |
| AGTCCATAAC | ATGCCATATC | TGGATTTTGT | GCTTAGNACC  | CTTAAATTGG  | AGCATTCTTN | 540 |
| ATTATGCATC | TAAATTTAAA | GGAGGTAATT | TTAAACCACT  | NCTTCNTTCC  | CTTTGGTTNA | 600 |
| CCATTTCAAT | ACCTNAACCA | AATTANNNG  | GNCANGCAAC  | ANNTAANTTC  | CTAGCNATAG | 660 |
| GGTNNTTAAT | NAAAGGGGTG | NTTTTNTCTT | GNNTNAGTTT  | TAATANCCCN  | CCNTNNAATT | 720 |
| TC         |            |            |             |             |            | 722 |

## (2) INFORMATION FOR SEQ ID NO:55:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1049 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
 (A) LIBRARY: LIVRTUT01  
 (B) CLONE: 1753185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

|             |            |            |             |            |            |      |
|-------------|------------|------------|-------------|------------|------------|------|
| GGTGGGCTGG  | TTCGGACGTG | GGTCGAGGCT | GTAGCAGGAC  | TCCAGGAAGA | TGTTACCGAG | 60   |
| TACTTCAGTG  | AATTCCCTAG | TGCAGGGGAA | CGGAGTCTTG  | AATTCCAGGG | ATGCGGCAAG | 120  |
| ACACACAGCC  | GGAGCGAAAC | GCTACAAATA | TCTGAGAAGG  | CTTTTCCGCT | TTCGGCAAAT | 180  |
| GGACTTTGAA  | TTTGCTGCCT | GGCAGATGCT | CTACCTGTTC  | ACATCCCCAC | AGAGAGTTTA | 240  |
| CAGAAATTTT  | CATTATCGAA | AACAGACGAA | GGACCAGTGG  | GCCAGAGATG | ACCCTGCTTT | 300  |
| CTTGGTCCTG  | TAAAGTATCT | GGCTCTGTGT | GTCCACTATA  | GGATTGGCT  | TTGTGCTGGA | 360  |
| CATGGGATTC  | TTTGAGACAA | TAAAGCTTCT | CCTTTGGGTT  | GTACTCATAG | ATTGTGTAGG | 420  |
| CGTTGGTCTT  | CTGATAGCAA | CTTTAATGTG | GTTTCATCTCT | AACAAGTATT | TAGTGAAACG | 480  |
| ACAGAGCAGA  | GACTATGATG | TGGAATGGGG | CTATGCTTTT  | GATGTGCATC | TCAATGCTTT | 540  |
| TTATCCACTC  | CTGGTCATTT | TGCATTTTAT | CCAGCTTTT   | TTCATCAACC | ATGTTATCCT | 600  |
| GACAGACACA  | TTTATTGGAT | ATTTAGTTGG | AAATACCTTA  | TGGTTGGTTG | CAGTTGGCTA | 660  |
| TTATATCTAT  | GTAACCTTCC | TGGGATACAG | TGCATTGCCA  | TTTTTGAAAA | ATACAGTAAT | 720  |
| TCTTCTGTAT  | CCATTTGCAC | CTCTGATTCT | GCTCTACGGG  | CTTTCCCTGG | CACTGGGATG | 780  |
| GAACCTTCACC | CATACCTCTT | GTTCTTTCTA | TAAGTACAGA  | GTGAAATAAA | AAGTGAGAAG | 840  |
| AAGATTCAAT  | CGTAACTGTG | TCAACAGTAT | TGTGAAGTGA  | TCATTCTCTG | TAAACTTTGT | 900  |
| AAATAAACTA  | TCATCTTTGT | AGATATCTTA | AAGGTGTAAA  | GTTTGCAAAT | TTGAAGAAAT | 960  |
| ATATATTAAC  | ACTGTGGTCA | GGTACATTCC | TTAAACTAA   | TTAAATGTAC | ATTTCTATAA | 1020 |
| TAAATATTTT  | TTAAACTAAA | AAAAAAAAA  |             |            |            | 1049 |

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 664 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
 (A) LIBRARY: COLNNOT08  
 (B) CLONE: 1844162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| ACAAGGGCTG  | CCGCTGCTGC | CGCCGCCGCC | TCGGGTCGTG | GAGNCANGAG | NGACGGTCAC | 60  |
| CGCCATGGCA  | GGCATCAAAG | CTTTGATTAG | TTTGTCTTT  | GGAGGAGCAA | TCGGACTGAT | 120 |
| GTTTTTGATG  | CTTGGATGTG | CCCTTCCAAT | ATACAACAAA | TACTGGCCCC | TCTTTGTTCT | 180 |
| ATTTTTTTTAC | ATCCTTTCAC | CTATTCCATA | CTGCATAGCA | AGAAGATTAG | TGGATGATAC | 240 |
| AGATGCTATG  | AGTAACGCTT | GTAAGGAAC  | TGCCATCTTT | CTTACAACGG | GCATTGTCTG | 300 |
| GTCAGCTTTT  | GGACTCCCTA | TTGTATTTGC | CAGAGCACAT | CTGATTGAGT | GGGGAGCTTG | 360 |
| TGCACTTGTT  | CTCACAGGAA | ACACAGTCAT | CTTTGCAACT | ATACTAGGCT | TTTTCTTGGT | 420 |
| CTTTGGAAGC  | AATGACGACT | TCAGCTGGCA | GCAGTGCTGA | AAAGAAATTA | CTGAATATT  | 480 |
| GTCAAATGGA  | CTTCCTGTCA | TTTGTTGGCC | ATTCACGCAC | ACAGGAGATG | GGGCAGTTAA | 540 |
| TGCTGAATGG  | TATAGCAAGC | CTCTTGGGGG | TATTTTAGGT | GCTCCCTTCT | CACTTTTATT | 600 |
| GTAAGCATAC  | TATTTTCACA | GAGACTTGCT | GAAGGATTAA | AAGGATTTTC | TCTTTTGGNA | 660 |
| AAAA        |            |            |            |            |            | 664 |

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 590 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: COLNNOT08

(B) CLONE: 1844338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| CGGCGCCTTG | AGGTAAGCTA | CAGGCAACAC | CACTTCCGCG | TTTCTCTTGC | GCCCTGGTCC | 60  |
| AAGATGGCGG | ATGAAGCCAC | GCGACGTGTT | GTGTCTGAGA | TCCCGGTGCT | GAAGACTAAC | 120 |
| GCCGGACCCC | GAGATCGTGA | GTTGTGGGTG | CAGCGACTGA | AGGAGGAATA | TCAGTCCCTT | 180 |
| ATCCGGTATG | TGGAGAACAA | CAAGAATGCT | GACAACGATT | GGTTCGACT  | GGAGTCCAAC | 240 |
| AAGGAAGGAA | CTCGGTGGTT | TGGAAAATGC | TGGTATATCC | ATGACCTCCT | GAAATATGAG | 300 |
| TTTGACATCG | AGTTTGACAT | TCCTATCACA | TATCCTACTA | CTGCCCCAGA | AATTGCAGTT | 360 |
| CCTGAGCTGG | ATGGAAAGAC | AGCAAAGATG | TACAGGGGTG | GCAAAATATG | CCTGACGGAT | 420 |
| CATTTCAAAC | CTTTGTGGGC | CAGGAATGTG | CCCAAATTTG | GACTAGCTCA | TCTCATGGCT | 480 |
| CTGGGGCTGG | GTCCATGGCT | GGCAGTGGAA | ATCCCTGATC | TGATTCAGAA | GGGCGTCATC | 540 |
| CAACACAAAG | AGAAATGCAA | CCAATGAAGA | ATCAAGCCAC | TGAGGCAGGG |            | 590 |

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 480 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: LUNGFET03

(B) CLONE: 1853104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| GGACTCGCTA | AGTGTTCGCT | ACGCGGGGCT | ACCGGATCGG | TCGGAAATGG | CAGANGTGGA | 60  |
| GGAGACACTG | AAGCGACTGC | AGAGCCAGAN | GGGAGTGCAG | GGAATCATCG | TCGTGAACAC | 120 |
| AGAAGGCATT | CCCATCAAGA | GCACCATGGA | CAACCCCAAC | ACCACCCAGT | ATGCCAGCCT | 180 |
| CATGCACAGC | TTCATCCTGA | AGGCACGGAG | CACCGTGCCT | GACATCGACC | CCCAGAACGA | 240 |
| TCTCACCTTC | CTTCGAATTC | GCTCCAAGAA | AAATGAAATT | ATGGTTGCAC | CAGATAAAGA | 300 |
| CTATTTCTTG | ATGTGTGATC | AGAATCCAAC | CGAATAAGCC | ACTCTCTTGG | CTCCCTGTGT | 360 |
| CATTCTTAA  | TTTAATGCCC | CCCAAGAATG | TTAATGTCAA | TCATGTCACT | GGACTAGCAC | 420 |
| ATGGCAGTCG | CTTGGAACCC | ACTCACACCA | ATCCAGTGAC | CGTGTGTGGG | CTGGCGGCTC | 480 |

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1121 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: PROSNOT18

(B) CLONE: 1858616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

|            |             |             |            |            |            |     |
|------------|-------------|-------------|------------|------------|------------|-----|
| GGACGGAGGT | CAGTGA CTCT | GGGGTCTCGG  | GAACCCGGAG | ACGAAGGAAG | ACACCGTGTT | 60  |
| CCTTAAGAGG | GAGTATACGT  | TTCCTCGCCA  | TTTATCCAAT | GGAGTTTCCT | CTTACCTACT | 120 |
| TAACAGGAAC | AGGGAAAGGG  | TGTCCCCCAA  | CGGTACGGCT | GCCCCGCTC  | TTCCTGGGGG | 180 |
| CCCACACGTG | TTACAGGAAG  | TGGGTAAGGG  | TAATATGGAG | GAGCTTCCGG | CAGCCCCCGG | 240 |
| CGGCTGAAAG | CGGGGGCAGA  | AGTGCTGGTC  | TCGGTCTGGG | TTCCGGGCTT | GGTCCCACCG | 300 |
| AGGCGGCGAC | TGCGGTAGGA  | GGGAAGAGGT  | TTTGGACGCG | CTGGCCTCCC | GCCGCTGTGC | 360 |
| ATTGCAGCAT | TATTTCACTT  | CAAAATGAAC  | TATATGCCTG | GCACCGCCAG | CCTCATCGAG | 420 |
| GACATTGACA | AAAAGCACTT  | GGTTC TGCTT | CGAGATGGAA | GGACACTTAT | AGGCTTTTAA | 480 |

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| AGAAGCATTG | ATCAATTTGC | AAACTTAGTG | CTACATCAGA | CTGTGGAGCG | TATTCATGTG | 540  |
| GGCAAAAAAT | ACGGTGATAT | TCCTCGAGGG | ATTTTGTGG  | TCAGAGGAGA | AAATGTGGTC | 600  |
| CTACTAGGAG | AAATAGACTT | GGAAAAGGAG | AGTGACACAC | CCCTCCAGCA | AGTATCCATT | 660  |
| GAAGAAATTC | TAGAAGAACA | AAGGGTGGAA | CAGCAGACCA | AGCTGGAAGC | AGAGAAGTTG | 720  |
| AAAGTGCAGG | CCCTGAAGGA | CCGAGGTCTT | TCCATTCCTC | GAGCAGATAC | TCTTGATGAG | 780  |
| TACTAATCTT | TTGCCCAGAG | GCTGTTGGCT | CTTGAAGAGT | AGGGGCTGTC | ACTGAGTGAA | 840  |
| AGTGACATCC | TGGCCACCTC | ACGCATTTGA | TCACAGACTG | TAGAGTTTTG | AAAAGTCACT | 900  |
| TTTATTTTTA | ATTATTTTAC | ATATGCAACA | TGAAGAAATC | GTGTAGGTGG | GTTTTTTTTT | 960  |
| TAATAACAAA | ATCACTGTTT | AAAGAAACAG | TGGCATAGAC | TCCTTCACAC | ATCACTGTGG | 1020 |
| CACCAGCAAC | TACTTCTTTA | TATTGTTCTT | CATATCCCAA | ATTAGAGTTT | ACAGGGACAG | 1080 |
| TCTTCATTTA | CTTGTAATA  | AAATATGAAT | CTCAAAAGTG | T          |            | 1121 |

## (2) INFORMATION FOR SEQ ID NO:60:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: UCMCL5T01
- (B) CLONE: 1969807

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

|            |            |            |             |            |             |     |
|------------|------------|------------|-------------|------------|-------------|-----|
| GAGAAGGTGC | TTTAGTCTGA | AGATGGCGGC | CTCAGCAGCG  | AGAGGTGCTG | CGGCGCTGCG  | 60  |
| TAGAAGTATC | AATCAGCCGG | TTGCTTTTGT | GAGAAGAATT  | CCTTGGACTG | CGGCGTCGAG  | 120 |
| TCAGTGAAA  | GAACACTTTG | CACAGTTCGG | CCATGTCAGA  | AGGTGCATTT | TACCTTTTGA  | 180 |
| CAAGGAGACT | GGCTTTCACA | GAGGTTTGGG | TTGGGTTTCAG | TTTTCTTCAG | AAGAAGGACT  | 240 |
| TCGGAATGCA | CTACAACAGG | AAAATCATAT | TATAGATGGA  | GTAAAGGTCC | AGGTTTCACAC | 300 |
| TAGAAGGCCA | AAACTTCCGC | AAACATCTGA | TGATGAAAAG  | AAAGATTTTT | GAGACTGCAG  | 360 |
| CCTATTAATA | AAGTTAACAT | AACTGAAAAA |             |            |             | 390 |

## (2) INFORMATION FOR SEQ ID NO:61:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 679 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: UCMCL5T01
- (B) CLONE: 1971003

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

|             |            |            |             |             |            |     |
|-------------|------------|------------|-------------|-------------|------------|-----|
| CTCGCCTGGG  | CTGTTTCCCG | GCTTCATTTT | TCCCAGACTCA | GCTTCCCACC  | CTGGGCTTTC | 60  |
| CGAGGTGCTG  | TCGCCGCTGT | CCCCACCACT | GCAGCCATGA  | TCTCCTTAAC  | GGACACGCAG | 120 |
| AAAATTGGAA  | TGGGATTAAC | AGGATTTGGA | GTGTTTTTCC  | TGTTCTTTGG  | AATGATTCTC | 180 |
| TTTTTTTGACA | AAGCACTACT | GGCTATTGGA | AATGTTTTAT  | TTGTAGCCGG  | CTTGGCTTTT | 240 |
| GTAATTGGTT  | TAGAAAGAAC | ATTCAGATTC | TTCTTCCAAA  | AACATAAAAT  | GAAAGCTACA | 300 |
| GGTTTTTTTC  | TGGGTGGTGT | ATTTGTAGTC | CTTATTGGTT  | GGCCTTTGAT  | AGGCATGATC | 360 |
| TTCGAAATTT  | ATGGATTTTT | TCTCTTGTTT | AGGGGCTTCT  | TTCCTGTCGT  | TGTTGGCTTT | 420 |
| ATTAGAAGAG  | TGCCAGTCCT | TGGATCCCTC | CTAAATTTAC  | CTGGAATTAG  | ATCATTTGTA | 480 |
| GATAAAGTTG  | GAGAAAGCAA | CAATATGGTA | TAACAACAAG  | TGAATTTGAA  | GACTCATTTA | 540 |
| AAATATTGTG  | TTATTTATAA | AGTCATTTGA | AGAATATTCA  | GCACAAAATT  | AAATTACATG | 600 |
| AAATAGCTTG  | TAATGTTCTT | TACAGGAGTT | TAAAACGTAT  | AAAACCTCACT | TGTATAATAA | 660 |
| ACAGTTTTTT  | AGGGATTTT  |            |             |             |            | 679 |

## (2) INFORMATION FOR SEQ ID NO:62:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: UCMCL5T01
- (B) CLONE: 1972328

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| GGCGTTAATG | GAGCAGCAGC  | AGCAGCAACT | GCGAAACCTG | CGTGACTTCC | TGTTGGTCTA | 60  |
| CAATCGGATG | ACAGAACTGT  | GTTTCCAGCG | CTGTGTGCCC | AGCCTGCACC | ACCGAGCTCT | 120 |
| GGACGCTGAG | GAGGAGGCCCT | GCCTGCACAG | CTGTGCTGGG | AAACTCATCC | ATTCTAACCA | 180 |
| CCGCCTCATG | GCCGCTTACG  | TGCACCTCAT | GCCCGCCCTG | GTCCAGCGCC | GCATCGCAGA | 240 |
| CTACGAGGCT | GCCTCGGCCG  | CGCCAGGTAT | TCCTGCAGAA | CAGACCAGAG | ACTCGCCATC | 300 |
| AGGCAGCTAG | CCGTCCCTGG  | CCCCTGGAGA | GAAGGTGCTT | GGATGGGCTC | CTCTATGGAC | 360 |
| CTTGGGCTTA | TCTAAATGTG  | TACAGAGAGA | TTGAGCTTGA | AAGCTGGGTG | CTGTTGCTCC | 420 |
| TTTCTTGGA  | GCCAATAAAC  | CCGTTTTTAC | AGTCTGAAAA | AAAAAAA    |            | 467 |

## (2) INFORMATION FOR SEQ ID NO:63:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BEPINOT01
- (B) CLONE: 2057883

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| GCCGGGTGCT | GATGCGAGTC | GGTGGCAGCG | AGGACATTTT | CTGACTCCCT | GGCCCCTGAC | 60   |
| ACGGCTGCAC | TTTCCATCCC | GTCGCGGGGC | CGGCCGCTAC | TCCGGCCCCA | GGATGCAGAA | 120  |
| TGTGATTAAT | ACTGTGAAGG | GAAAGGCACT | GGAAGTGGCT | GAGTACCTGA | CCCCGGTCCT | 180  |
| CAAGGAATCA | AAGTTTAAGG | AAACAGGTGT | AATTACCCCA | GAAGAGTTTG | TGGCAGCTGG | 240  |
| AGATCACCTA | GTCCACCAC  | GTCCAACATG | GCAATGGGCT | ACAGGGGAAG | AATTGAAAGT | 300  |
| GAAGGCATAC | CTACCAACAG | GCAAACAATT | TTTGGTAACC | AAAAATGTGC | CGTGCTATAA | 360  |
| GCGGTGCAAA | CAGATGGAAT | ATTCAGATGA | ATTGGAAGCT | ATCATTGAAG | AAGATGATGG | 420  |
| TGATGGCGGA | TGGGTAGATA | CATATCACAA | CACAGGTATT | ACAGGAATAA | CGGAAGCCGT | 480  |
| TAAAGAGATC | ACACTGGAAA | ATAAGGACAA | TATAAGGCTT | CAAGATTGCT | CAGCACTATG | 540  |
| TGAAGAGGAA | GAAGATGAAG | ATGAAGGAGA | AGCTGCAGAT | ATGGAAGAAT | ATGAAGAGAG | 600  |
| TGGATTGTTG | GAAACAGATG | AGGCTACCCT | AGATACAAGG | AAAATAGTAG | AAGCTTGTA  | 660  |
| AGCCAAAACT | GATGCTGGCG | GTGAAGATGC | TATTTTGCAA | ACCAGAACTT | ATGACCTTTA | 720  |
| CATCACTTAC | GATAAATATT | ACCAGACTCC | ACGATTATGG | TTGTTTGGCT | ATGATGAGCA | 780  |
| ACGGCAGCCT | TTAACAGTTG | AGCACATGTA | TGAAGACATC | AGTCAGGATC | ATGTGAAGAA | 840  |
| AACAGTGACC | ATTGAAAATC | ACCTCATCT  | GCCACCACCT | CCCATGTGTT | CAGTTCACCC | 900  |
| ATGCAGGCAT | GCTGAGGTGA | TGAAGAAAAT | CATTGAGACT | GTGCAGAAG  | GAGGGGGAGA | 960  |
| ACTTGAGT   | CATATGTATC | TTCTTATTTT | CTTGAAATTT | GTACAAGCTG | TCATTCCAAC | 1020 |
| AATAGAATAT | GACTACACAA | GACACTTCAC | AATGTAATGA | AGAGAGCATA | AAATCTATCC | 1080 |
| TAATTATTGG | TTCTGATTTT | TAAAGAATTA | ACCCATAGAT | GTGACCATTG | ACCATATTCA | 1140 |
| TCAATATATA | CAGTTTCTCT | AATAAGGGAC | TTATATGTTT | ATGCATTAAA | TAAAAATATG | 1200 |
| TTCCACTACC | AGCCTTACTT | GTTTAATAAA | AATCAGTGCA | AAGAGGA    |            | 1247 |

## (2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: ISLTNOT01
- (B) CLONE: 2075409

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| TGGCTCAGGT | GGACTCCGGG | CTGGAGCTGT | CCTGGGGGAG | CTTGTTTGCG | GCAGCGGCTG | 60  |
| CTGNTGCCAC | TGCTGTGCTG | GGGGCCCGGT | CGCCAGGCAA | AAAGCCCTCC | CACGTTTGAG | 120 |
| GGGAGTCATG | AGCCGTTTCC | TGAATGTGTT | AAGAAGTTGG | CTGGTTATGG | TGTCCATCAT | 180 |
| AGCCATGGGG | AACACGCTGC | AGAGCTTCCG | AGACCACACT | TTTCTCTATG | AAAAGCTCTA | 240 |
| CACTGGCAAG | CCAAACCTTG | TGAATGGCCT | CCAAGCTCGG | ACCTTTGGGA | TCTGGACGCT | 300 |
| GCTCTCATCA | GTGATTCGCT | GCCTCTGTGC | CATTGACATT | CACAACAAGA | CGCTCTATCA | 360 |
| CATCACACTC | TGGACCTTCC | TCCTTGCCCT | GGGGCATTTT | CTCTCTGAGT | TGTTTGTCTA | 420 |
| TGGAAGTGCA | GCTCCCACGA | TTGGCGTCCT | GGCACCCCTG | ATGGTGCCAA | GTTTCTCCAT | 480 |
| CCTGGGTATG | CTGGTCGGGC | TCCGGTATCT | AGAAGTAGAA | CCAGTATCCA | GACAGAAGAA | 540 |
| GAGAACTGA  | GGCCAGCATT | ATCACCTCCA | GGACTTTCTC | GTTTTCACCC | TTGGCCATCT | 600 |
| TCTTCCTTCG | TCGTCTCTCC | TCTTTAATTT | CTTTTCTATT | CCATCATCTG | CCCTTTTATT | 660 |
| CACTTTTAAG | CCTCTTTTTT | TAATTTTAA  | AATTTAAAGA | TATGCATACT | GAAAAGTATA | 720 |
| TAACATGTAC | GTACAATTTA | AAGAATAATT | TTAAAGTGAA | TACTACGTAA | CTC        | 773 |

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 577 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRAITUT02
- (B) CLONE: 2095728

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| GCGCCGAGGG | GCTGCGAGAG  | TGACCGCGGC | TGCGAGAGTG | ACCGCGGCTG | CTCCAGCGCT | 60  |
| GACGCCGAGC | CATGGCGGAC  | GAGGAGCTTG | AGGCGCTGAG | GAGACAGAGG | CTGGCCGAGC | 120 |
| TGCAGGCCAA | ACACGGGGAT  | CCTGGTGATG | CGGCCCAACA | GGAAGCAAAG | CACAGGGAAG | 180 |
| CAGAAATGAG | AAACAGTATC  | TTAGCCCAAG | TTCTGGATCA | GTCGGCCCCG | GCCAGGTAA  | 240 |
| GTAACCTAGC | ACTTGTAAG   | CCTGAAAAAA | CTAAAGCAGT | AGAGAATTAC | CTTATACAGA | 300 |
| TGGCAAGATA | TGGACAACCTA | AGTGAGAAGG | TATCAGAACA | AGGTTTAATA | GAAATCCTTA | 360 |
| AAAAAGTAAG | CCAACAAACA  | GAAAAGACAA | CAACAGTGAA | ATTCAACAGA | AGAAAAGTAA | 420 |
| TGGACTCTGA | TGAAGATGAC  | GATTATTGAA | CTACAAGTGC | TCACAGACTA | GAAGTTAACG | 480 |
| GAACAAGTCT | AGGACAGAAG  | TTAAGATCTG | ATTATTTACT | TTGTTTATTG | TCTATATGCC | 540 |
| TTTTAAAAAA | ATAAAGTTGT  | TATGCAAATT | AAATAAC    |            |            | 577 |

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 661 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRAITUT02

(B) CLONE: 2100016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| GGCCGGCTGA | CCCCACCTCG | CTGGGCCCTC | CCTGGCGCCC | CGCCTTGGGC | GGCGGCGAGC | 60  |
| GCGCGGGCCG | CCATGTCGTA | CATGCTCCCG | CACCTGCACA | ACGGCTGGCA | GGTGGACCAG | 120 |
| GCCATCCTCT | CGGAGGAGGA | CCGCGTGCTC | GTCATCCGCT | TCGGCCACGA | CTGGGATCCT | 180 |
| ACGTGCATGA | AGATGGACGA | GGTCCTGTAC | AGCATCGCCG | AGAAGGTTAA | AAATTTTGCA | 240 |
| GTTATTTATC | TTGTGGATAT | TACAGAAAGT | CCTGACTTCA | ACAAAATGTA | TGAGTTATAC | 300 |
| GATCCATGTA | CTGTCATGTT | TTTCTTCAGG | AACAAGCACA | TCATGATTGA | CTTGGGGACT | 360 |
| GGCAACAACA | ACAAGATTAA | CTGGGCCATG | GAGGACAAGC | AGGAGATGGT | GGACATCATC | 420 |
| GAGACGGTGT | ACCGCGGGGC | CCGCAAAGGC | CGCGGCCTGG | TGGTGTCCCC | CAAGGACTAC | 480 |
| TCCACCAAGT | ACCGCTACTG | AGGCGCCCTC | AGTCTGCGCG | GATAAATGTC | GTGGAGCCCT | 540 |
| TTTTGTATGG | AAACGTTTTA | AGCTATTTAA | AGCCTTTGGA | AAATACAGGA | AGCTCCAGGG | 600 |
| CTGGAGCACC | TCTGAGATGG | AATTGATAAC | ATGGTCTTAA | CTACCGAAA  | TAAACAAGCA | 660 |
| C          |            |            |            |            |            | 661 |

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1570 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: KIDNNOT05
- (B) CLONE: 2126751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

|            |            |            |            |             |             |      |
|------------|------------|------------|------------|-------------|-------------|------|
| CCGGAAAGTC | TTCGCGGCGG | AGGCCCCGGC | AACTCTTTTG | AATGGAATCG  | GGCTGATTCA  | 60   |
| TCGCCGGTTT | GCAGACTGAG | CCGCGTCGGG | TGTGCGCCGC | TGCTGCTGTT  | GCCTCTGTCT  | 120  |
| TCGCGTCACC | ACAGAGGCAA | GACAAGGGTC | CATATCGCGG | CATCCGGCTC  | CCGCCCCGTCT | 180  |
| TCAGGAGAGA | AAGAAAAAAT | AAAATATACT | TGGGGAAGTT | GTACCTGCCA  | GAATTAGCAA  | 240  |
| GAGCTTTCTT | TAAGAAGACA | TTTGTCAAAC | TCAACAAATT | GAAGGTTAAC  | ACCTTAAGAG  | 300  |
| TTGTAGTTAC | TGACCAGAAA | TATGGACAGA | CTTCTTAGAC | TTGGAGGAGG  | TATGCCTGGA  | 360  |
| CTGGGCCAGG | GGCCACCTAC | AGATGCTCCT | GCAGTGGACA | CAGCAGAACA  | AGTCTATATC  | 420  |
| TCTTCCCTGG | CACGTGTTAA | AATGTTAAAA | CATGGCCGTG | CTGGAGTTCC  | AATGGAAGTT  | 480  |
| ATGGGTTTGA | TGCTTGAGGA | ATTTGTTGAT | GATTATACCG | TCAGAGTGAT  | TGATGTGTTT  | 540  |
| GCTATGCCAC | AGTCAGGAAC | AGGTGTCAGT | GTGGAGGCAG | TTGATCCAGT  | GTTCCAAGCT  | 600  |
| AAAATGTTGG | ATATGTTGAA | GCAGACAGGA | AGGCCGGAGA | TGGTTGTTGG  | TTGGTATCAC  | 660  |
| AGTCACCCTG | GCTTTGGTTG | TTGGCTTTCT | GGTGTGGATA | TCAACACTCA  | GCAGAGCTTT  | 720  |
| GAAGCCTTGT | CGGAGAGAGC | TGTGGCAGTG | GTTGTGGATC | CCATTCAGAG  | TGTAAAAGGA  | 780  |
| AAGGTTGTTA | TTGATGCCTT | CAGATTGATC | AATGCTAATA | TGATGGTCTT  | AGGACATGAA  | 840  |
| CCAAGACAAA | CAACTTCGAA | TCTGGGTCAC | TAAACAAGC  | CATCTATCCA  | GGCATTAATT  | 900  |
| CATGGACTAA | ACAGACATTA | TTACTCCATT | ACTATTAAT  | ATCGGAAAAA  | TGAAGTGGAA  | 960  |
| CAGAAGATGT | TGCTAAATTT | GCATAAGAAG | AGTTGGATGG | AAGGTTTGAC  | ACTTCAGGAC  | 1020 |
| TACAGTGAAC | ATTGTAAACA | CAATGAATCA | GTGGTAAAAG | AGATGTTGGA  | ATTAGCCAAG  | 1080 |
| AATTACAATA | AGGCTGTAGA | AGAAGAAGAT | AAGATGACAC | CTGAACAGCT  | GGCAATAAAG  | 1140 |
| AATGTTGGCA | AGCAGGACCC | CAAACGTCAT | TTGGAGGAAC | ATGTGGATGT  | ACTTATGACC  | 1200 |
| TCAAATATTG | TCCAGTGTTT | AGCAGCTATG | TTGGATACTG | TCGTATTTAA  | ATAAAGCAAC  | 1260 |
| GAAAAACGCT | ATTAATGATG | CCTTCAGTGT | ATATTCCTCT | GTTGTTCCCTA | ATGCTCAAAA  | 1320 |
| TCAAGGGACC | TCTGAAGGTG | TACTTGGCTA | AATGTAAGAC | ATCTGGCATC  | ATTTGCAGCA  | 1380 |
| CTGTAACACC | TTCAGTCTCA | GTTGTGCAAT | TACTTCTGTT | TCTTTAGTCA  | GGGTCTTTGC  | 1440 |
| AGATTCTAAA | GTTATACATG | AATACATCAA | AGTGGACAAA | TTTTGTTAAG  | ATCCCATTTA  | 1500 |
| ATATTTGAAA | AAATCAGTAG | CACAAATATA | TTTTGATTGT | CACTTACAAA  | ATAAAATACA  | 1560 |
| TTTACAGTCT |            |            |            |             |             | 1570 |

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SININOT01
- (B) CLONE: 2179882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

|            |             |            |            |            |             |      |
|------------|-------------|------------|------------|------------|-------------|------|
| AGCCGCCGCC | ATGAAGGCCG  | TGGTGCAGCG | CGTCACCCGG | GCCAGCGTCA | CAGTTGGAGG  | 60   |
| AGAGCAGATT | AGTGCCATTG  | GAAGGGGCAT | ATGTGTGTTG | CTGGGTATTT | CCCTGGAGGA  | 120  |
| TACGCAGAAG | GAAC TGGAAC | ACATGGTCCG | AAAGATTCTA | AACCTGCGTG | TATTTGAGGA  | 180  |
| TGAGAGTGGG | AAGCACTGGT  | CGAAGAGTGT | GATGGACAAA | CAGTACGAGA | TTCTGTGTGT  | 240  |
| CAGCCAGTTT | ACCCTCCAGT  | GTGTCTTGAA | GGGAAACAAG | CCTGATTTCC | ACCTAGCAAT  | 300  |
| GCCCACGGAG | CAGGCAGAGG  | GCTTCTACAA | CAGCTTCCTG | GAGCAGCTGC | GTA AACATA  | 360  |
| CAGGCCGGAG | CTTATCAAAG  | ATGGCAAGTT | TGGGGCCTAC | ATGCAGGTGC | ACATTCAGAA  | 420  |
| TGATGGGCCT | GTGACCATAG  | AGCTGGAATC | GCCAGCTCCC | GGCACTGCTA | CCTCTGACCC  | 480  |
| AAAGCAGCTG | TCAAAGCTCG  | AAAAACAGCA | GCAGAGGAAA | GAAAAGACCA | GAGCTAAGGG  | 540  |
| ACCTTCTGAA | TCAAGCAAGG  | AAAGAAACAC | TCCCCGAAAA | GAAGACCGCA | GTGCCAGCAG  | 600  |
| CGGGGCTGAG | GGCGACGTGT  | CCTCTGAACG | GGAGCCGTAG | CTCAGGAGGC | AGAATTCAGT  | 660  |
| GTGTTATCAT | TGGGCAGAAC  | TGGATCCTGA | AAAATTCAAG | ATGCTAAGCA | CCTACACTAC  | 720  |
| TTTAAGAATT | TGGAATGAA   | ACATGAAGAG | GAAGACAGAA | ATAAGAATTT | GGGAACCTGA  | 780  |
| ATAGCTCTGC | AAAAAACACC  | AAAGGACCGT | TTTATCGTTT | TCTGTTGTTG | CTGTGGTGGA  | 840  |
| GTGATGCAGT | GGGCACTGCC  | GGTGGGGCAG | GGGGCGGGTG | CGCATGTGGT | AGAAGGTGTG  | 900  |
| CGCTCGTGCC | TCCCCACAG   | AAAGGCTTTG | TTGGTTTCTA | CCACATCTTG | GCTTGCTTTT  | 960  |
| GGAACAGGCT | GGCCCCAGCA  | TCATTTGTCA | TCAAGTCCAC | TGTGGTGTAT | TCTGCGTGTC  | 1020 |
| CATGGCGGGG | GTTCTCCAAT  | ACACTCACAC | TGTCCATGTT | CTTTTTATTG | CCAGGGCCCCG | 1080 |
| TGTTGAAGTG | TCAAGAGAGC  | AATCATCAAT | GATAATGTAT | TGTGTGAGAC | CTTTGCATCT  | 1140 |
| TGTAAATTTT | CTCTTTTTTC  | TAAAAATAAA | TAATAATAAA | ATCCTAAATC | TCAAC       | 1195 |

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 714 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSNON01
- (B) CLONE: 2275119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| GGAAAGTTCC | CGAGAGCTTC  | CGGTGGCCGG | CTTAGTTAGG | AGCTATGGCT | AAACATCATC | 60  |
| CTGATTTGAT | CTTTTGCCGC  | AAGCAGGCTG | GTGTTGCCAT | CGGAAGACTG | TGTGAAAAAT | 120 |
| GTGATGGCAA | GTGTGTGATT  | TGTGACTCCT | ATGTGCGTCC | CTGCACTCTG | GTGCGCATAT | 180 |
| GTGATGAGTG | TAAC TATGGA | TCTTACCAGG | GGCGCTGTGT | GATCTGTGGA | GGACCTGGGG | 240 |
| TCTCTGATGC | CTATTATTGT  | AAGGAGTGCA | CCATCCAGGA | GAAGGACAGA | GATGGCTGCC | 300 |
| CAAAGATTGT | CAATCTGGGG  | AGCTCTAAGA | CAGACCTCTT | CTATGAACGC | AAAAAATACG | 360 |
| GCTTCAAGAA | GAGGTGATTG  | GTGGGGTGGC | CCCTTCCTCC | CCCCAACATC | AGTCTGCTGC | 420 |
| AGCTGCCAGA | AAACATGCCT  | ACTACTACCA | GCAGAAAGGG | AGCAGAGCCC | AGAGCATCAC | 480 |
| CAGGAGTGCC | TGCTAGTGTA  | CTGGCAGCTT | GCCACCCCTT | CCTCTCCCTT | CACCCAGACA | 540 |
| CGTGGTAGGG | ATGGAAAAGG  | ATTCTTCACA | GAGCACTCTG | GCACACCATA | TCGGAGAAAA | 600 |
| CTTGATAGAT | TAGTTAATGG  | TTTTTCTTGA | ATTCGAGAAG | CATAGATCTG | TTCTCCATAT | 660 |
| TGGTATGTTT | TCCCTCAACC  | AAGATCTTCT | AAAAAGAAAT | AATATTTTAG | TCTT       | 714 |

(2) INFORMATION FOR SEQ ID NO:70:



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSNON01
- (B) CLONE: 2278093

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

|            |             |             |             |             |            |      |
|------------|-------------|-------------|-------------|-------------|------------|------|
| CTGTTAATGG | CGGGCAGTAG  | CCGCTGTAGG  | GGATTGCAGA  | TAACCGCTTC  | CCGCACGGGG | 60   |
| AAAGTCTACC | CTGCCTGCCA  | CTTTCTGCTC  | GCCGTCAGCG  | CCGGAGCTCG  | CCAGCATGTC | 120  |
| TGTGGTACCG | CCCAATCGCT  | CGGCAGACCG  | GCTGGCCCCG  | GGGGGGTCAC  | TCAGTTCGGC | 180  |
| AACAAGTACA | TCCAGCAGAC  | GAAGCCCCCTC | ACCCTGGAGC  | GCACCATCAA  | CCTGTACCCT | 240  |
| CTTACCAATT | ATACTTTTGG  | TACAAAAGAG  | CCCCCTCTACG | AGAAGGACAG  | CTCTGTTGCA | 300  |
| GCCAGATTTT | AGCGCATGAG  | GGAAGAATTT  | GATAAAATTTG | GAATGAGGAG  | GACTGTAGAA | 360  |
| GGGGTTCTGA | TTGTACATGA  | GCACCGGCTA  | CCCCATGTGT  | TACTGCTGCA  | GCTGGGAACA | 420  |
| ACTTTCCTTA | AACCTACCTG  | TGGTGAACCT  | AACCCAGGAG  | AAGATGAAGT  | TGAAGGACTA | 480  |
| AAACGCTTAA | TGACAGAGAT  | ACTGGGTCGT  | CAGGATGGAG  | TTTTTGCAAGA | CTGGGTCATT | 540  |
| GACGATTGCA | TTGGTAACTG  | GTGGAGACCA  | AATTTTGAAC  | CTCCTCAGTA  | TCCATATATT | 600  |
| CCTGCACATA | TTACAAAGCC  | TAAGGAACAT  | AAGAAGTTGT  | TTCTGGTTCA  | GCTTCAAGAA | 660  |
| AAAGCCTTGT | TTGCAGTCCC  | TAAAAATTAC  | AAGCTGGTAG  | CTGCACCATT  | GTTTGAATTG | 720  |
| TATGACAATG | CACCAGGATA  | TGGACCCATC  | ATTCTAGTCT  | TCCCTCAGCT  | GTTGAGCAGG | 780  |
| TTCAATTTTA | TTTACAACCTG | AATTCCCTGC  | CAGTGGAGAA  | GTAAAAGAAG  | CCGCTTGTCT | 840  |
| CTGTGAGCAC | AGCTATATAC  | AGTGTAAGAT  | AAATGTGGTA  | GAAAAGTTTT  | TTTGTTTTTA | 900  |
| TCTCTTTTGC | GATCCCTAAA  | TTGCCACCTT  | TCTATTGTTT  | GAATAGTAAA  | ATTAATATGA | 960  |
| AGAACTAGAT | AGTGGTGTA   | ACAAATGTGA  | TAATGTTTAT  | TTACTTTTCG  | TTCTGCTCAT | 1020 |
| ACTTTTTTGT | ACAACATTAA  | AGAAAATGGA  | CTTTTTTTAT  | TTTAATTTCT  | CATTAACTT  | 1080 |
| CTAAAATTCT | TATAGGTGAG  | GATCATTTTT  | CCCCCACCT   | TAGGATGGTG  | AATGTTGCAA | 1140 |
| CACAATGACA | GG          |             |             |             |            | 1152 |

## (2) INFORMATION FOR SEQ ID NO:71:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 641 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: TESTTUT02
- (B) CLONE: 2345426

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| GAAAGCCCAG | CGATCCTTGG | CTCGGCCAGC | AACTTATGCG | CCCTTTACCT | GGAGCAGCCG | 60  |
| CTTCCGGTTC | CGGTAGCAGC | TAGTCACGCT | CGGTACCAGG | CGCAGATCAT | GGCAGGCAGC | 120 |
| CGGCTGGAAA | CCGTAGGGAG | CATCTTCTCT | CGGACTCGGG | ACCTGGTTCG | GGCCGGGGTG | 180 |
| CTGAAGGAGA | AGCCCCGTGT | GTTTGACGTA | TATGACGCCT | TTCCCCCGCT | GAGGGAGCCC | 240 |
| GTCTTCCAAA | GGCCTCGAGT | GCGATATGGC | AAAGCCAAAG | CTCCCATCCA | AGACATCTGG | 300 |
| TACCACGAGG | ATCGGATTAG | AGCGAAGTTT | TATTCAGTGT | ATGGGTCTGG | TCAAAGAGCT | 360 |
| TTTGATCTAT | TCAATCCAAA | CTTCAAGTCT | ACCTGTCAAC | GGTTTGTGGA | GAAGTACACT | 420 |
| GAGCTACAGA | AACTTGGAGA | AACAGATGAA | GAGAAGTTAT | TTGTGGAAAC | AGGGAAGGCT | 480 |
| TTATTGGGCA | GAAGGTGTCA | TTTTAAGACG | AGTAGGCGAG | AAGGACTCAA | CACGGAGGTA | 540 |
| GTCACGTTTC | CCGGAAATCC | GAACACTTGA | GTGTCAGACC | ACAGACTGCG | TTGGAAGAGA | 600 |
| ACGAGACTCA | GANAGAAGTT | CCACAAGGAC | CAGCATTTGG | A          |            | 641 |

## (2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 645 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: ADRENOT07
- (B) CLONE: 2364523

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| GGCGCCTTGA | GTCTCCGGGC | CGCCTTGCCA | TGGCTGCCCCG | TGGTGTCATC | GCTCCAGTTG | 60  |
| GCGAGAGTTT | GCGCTACGCT | GAGTACTTGC | AGCCCTCGGC  | CAAACGGCCA | GACGCCGACG | 120 |
| TCGACCAGCA | GAGACTGGTA | AGAAGTTTGA | TAGCTGTAGG  | ACTGGGTGTT | GCAGCTCTTG | 180 |
| CATTTGCAGG | TCGCTACGCA | TTTCGGATCT | GGAAACCTCT  | AGAACAAGTT | ATCACAGAAA | 240 |
| CTGCAAAGAA | GATTTCAACT | CCTAGCTTTT | CATCCTACTA  | TAAAGGAGGA | TTTGAACAGA | 300 |
| AAATGAGTAG | GCGAGAAGCT | GGTCTTATTT | TAGGTGTAAG  | CCCATCTGCT | GGCAAGGCTA | 360 |
| AGATTAGAAC | AGCTCATAGG | AGAGTCATGA | TTTTGAATCA  | CCCAGATAAA | GGTGGATCTC | 420 |
| CTTACGTAGC | AGCCAAAATA | AATGAAGCAA | AAGACTTGCT  | AGAAACAACC | ACCAAACATT | 480 |
| GATGCTTAAG | GACCACACTG | AAGGAAAAAA | AAAGAGGGGA  | CTTCGAAAAA | AAAAAAAGCC | 540 |
| CTGCAAAATA | TTCTAAAACA | TGGTCTTCTT | AATTTTCTAT  | ATGGATTGAC | CACAGTCTTA | 600 |
| TCTTCCGACC | ATTAAGCTGT | ATAACGAATA | AAATGTTAAT  | AGTCA      |            | 645 |

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 608 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THP1NOT03
- (B) CLONE: 2470912

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| GCGGCGGCGA | CGGAGGAGGA | GGATGGAGGC | GGTGGTGTTT | GTCTTCTCTC | TCCTCGATTG | 60  |
| TTGCGCGCTC | ATCTTCTCT  | CGGTCTACTT | CATAATTACA | TTGTCTGATT | TAGAATGTGA | 120 |
| TTACATTAAT | GCTAGATCAT | GTTGCTCAAA | ATTAAACAAG | TGGGTAATTC | CAGAATTGAT | 180 |
| TGGCCATACC | ATTGTCACTG | TATTACTGCT | CATGTCATTG | CACTGGTTCA | TCTTCTTCT  | 240 |
| CAACTTACCT | GTTGCCACTT | GGAATATATA | TCGATACATT | ATGGTGCCGA | GTGGTAACAT | 300 |
| GGGAGTGTTT | GATCCAACAG | AAATACACAA | TCGAGGGCAG | CTGAAGTCAC | ACATGAAAGA | 360 |
| AGCCATGATC | AAGCTTGTTT | TCCACTTGCT | CTGCTTCTTC | ATGTATCTTT | ATAGTATGAT | 420 |
| CTTAGCTTTG | ATAAATGACT | GAAGCTGGAG | AAGCCGTGGT | TGAAGTCAGC | CTACACTACA | 480 |
| GTGCACAGTT | GAGGAGCCAG | AGACTTCTTA | AATCATCCTT | AGAACCGTGA | CCATAGCAGT | 540 |
| ATATATTTTC | CTCTTGGAAC | AAAAAACTAT | TTTGTGCTGA | TTTTTACCAT | ATAAAGTATT | 600 |
| TAAAAAAC   |            |            |            |            |            | 608 |

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1553 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: CONUTUT01

(B) CLONE: 2507014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

|            |             |             |            |             |            |      |
|------------|-------------|-------------|------------|-------------|------------|------|
| GTGATTGTTA | TCTTGGTGCT  | GCAGAGGACA  | GCAGAAGAGG | AGATTGGGTC  | AGAAAACTGC | 60   |
| CCTGCCGCAC | CAGAGCACAG  | CGCACTAGTG  | GGACAGGGGT | CCTGACTCAG  | ACTTAACTGG | 120  |
| CTGTGTCTCG | TGGTTTTTCA  | CTGTCCTGGA  | AAAGGCCTGA | AGTGGCACTG  | AAATGAGGCA | 180  |
| TAGATGAGTC | CCCACGACAG  | TCCGGTTTGT  | AGATTCCCTG | ATCTGCAATT  | CTTCCCCTTC | 240  |
| CTTCATGGAT | TTGAAGGCTC  | TCCTTTCTTC  | CTTGAATGAC | TTTGCATCCC  | TCTCGTTTGC | 300  |
| TGAGAGTTGG | GACAATGTTG  | GATTACTGGT  | GGAACCAAGC | CCACCACATA  | CTGTAAATAC | 360  |
| ACTCTTCCTG | ACCAATGACC  | TGACTGAGGA  | AGTGATGGAG | GAGGTGCTGC  | AAAAGAAGGC | 420  |
| AGACCTCATT | CTCTCCTACC  | ATCCGCCTAT  | CTTCCGACCC | ATGAAGCGCA  | TAACCTGGAA | 480  |
| CACATGGAAG | GAGCGCCTGG  | TGATCCGGGG  | TCTGGAGAAC | AGAGTCGGTA  | TCTACTCTCC | 540  |
| TCATACAGCC | TATGATGCTG  | CGCCCCAGGG  | CGTCAACAAC | TGGTTGGCTA  | AAGGGCTTGG | 600  |
| AGCTTGTAAC | TCCAGGCCCA  | TACATCCTTC  | CAAAGCTCCC | AACTACCCTA  | CAGAGGGAAA | 660  |
| CCACCGAGTA | GAATTC AACG | TTA ACTACAC | CCAAGACCTG | GACAAAGTCA  | TGTCTGCAGT | 720  |
| GAAAGGAATT | GACGGTGTTT  | CTGTCACCTC  | TTTTTCTGCT | AGGACTGGTA  | ATGAGGAACA | 780  |
| AACACGGATT | AATCTGAATT  | GTACTCAGAA  | GGCTTTGATG | CAGGTGGTAG  | ATTTTCTTTC | 840  |
| CCGGAACAAA | CAACTTTATC  | AGAAGACGGA  | AATTCTGTCA | CTGGAGAAGC  | CTTTGCTTCT | 900  |
| ACATACTGGA | ATGGGACGGT  | TATGCACACT  | GGATGAATCT | GTCTCCCTGG  | CAACCATGAT | 960  |
| TGATCGAATA | AAAAGACACC  | TAAAACTATC  | TCATATTTCG | TTAGCCCTTG  | GGGTGGGGAG | 1020 |
| AACCTTAGAG | TCTCAAGTCA  | AAGTCGTGGC  | CCTGTGTGCT | GGTTC TGGGA | GCAGCGTTCT | 1080 |
| GCAGGGTGTT | GAGGCTGACC  | TTTACCTCAC  | AGGTGAGATG | TCCCATCATG  | ATACTTTGGA | 1140 |
| TGCTGCTTCC | CAAGGAATAA  | ATGTCATCCT  | CTGTGAACAC | AGCAACACTG  | AACGAGGCTT | 1200 |
| TCTTTCTGAC | CTTCGAGATA  | TGCTGGATTG  | TCACTTGGAG | AATAAGATAA  | ATATTATCCT | 1260 |
| ATCAGAGACT | GACAGGGACC  | CTCTTCAGGT  | GGTATAATTG | CAGAAACATC  | AGGATAACAC | 1320 |
| ATTCCTACAA | ATCAGCTGGA  | TGCCCAACTT  | AAATTTGTAA | CATGAGTCAG  | TGGGACTGGT | 1380 |
| GTGCTTCCAG | AGAGTGTCTT  | CGAGGGTATC  | ATCATTTCCG | GTTTGTTAAT  | CTTATTACAC | 1440 |
| AAATGTTCTA | TCGCTCGTAA  | GGTAAAAC TG | TAATATAACT | ACCATATTAA  | ATAACAAATG | 1500 |
| TTCATTATAA | ACTCTAGGAA  | AGATTGAATA  | AAATCTGTTT | ACTTAACATT  | CAA        | 1553 |